

06442439.1.1399

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 102

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: DP2.5(APC)

(ix) FEATURE:

(A) NAME/KEY: CDS

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(B) LOCATION: 34.8562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGACTCGGAA	ATGAGGTCCA	AGGGTAGCCA	AGG	ATG	GCT	GCA	GCT	TCA	TAT	GAT	54
			Met	Ala	Ala	Ala	Ser	Tyr	Asp		
			1				5				
CAG TTG TTA AAG CAA GTT GAG GCA CTG AAG ATG GAG AAC TCA AAT CTT	102										
Gln Leu Leu Lys Gln Val Glu Ala Leu Lys Met Glu Asn Ser Asn Leu											
	10	15	20								
CGA CAA GAG CTA GAA GAT AAT TCC AAT CAT CTT ACA AAA CTG GAA ACT	150										
Arg Gln Glu Leu Glu Asp Asn Ser Asn His Leu Thr Lys Leu Glu Thr											
	25	30	35								
GAG GCA TCT AAT ATG AAG GAA GTA CTT AAA CAA CTA CAA GGA AGT ATT	198										
Glu Ala Ser Asn Met Lys Glu Val Leu Lys Gln Leu Gln Gly Ser Ile											
	40	45	50								
GAA GAT GAA GCT ATG GCT TCT TCT GGA CAG ATT GAT TTA TTA GAG CGT	246										
Glu Asp Glu Ala Met Ala Ser Ser Gly Gln Ile Asp Leu Leu Glu Arg											
	60	65	70								
CTT AAA GAG CTT AAC TTA GAT AGC AGT AAT TTC CCT GGA GTA AAA CTG	294										
Leu Lys Glu Leu Asn Leu Asp Ser Ser Asn Phe Pro Gly Val Lys Leu											
	75	80	85								
CGG TCA AAA ATG TCC CTC CGT TCT TAT GGA AGC CGG GAA GGA TCT GTA	342										
Arg Ser Lys Met Ser Leu Arg Ser Tyr Gly Ser Arg Glu Gly Ser Val											
	90	95	100								
TCA AGC CGT TCT GGA GAG TGC AGT CCT GTT CCT ATG GGT TCA TTT CCA	390										
Ser Ser Arg Ser Gly Glu Cys Ser Pro Val Pro Met Gly Ser Phe Pro											
	105	110	115								
AGA AGA GGG TTT GTA AAT GGA AGC AGA GAA AGT ACT GGA TAT TTA GAA	438										
Arg Arg Gly Phe Val Asn Gly Ser Arg Glu Ser Thr Gly Tyr Leu Glu											
	120	125	130								
GAA CTT GAG AAA GAG AGG TCA TTG CTT CTT GCT GAT CTT GAC AAA GAA	486										
Glu Leu Glu Lys Glu Arg Ser Leu Leu Leu Ala Asp Leu Asp Lys Glu											
	140	145	150								
GAA AAG GAA AAA GAC TGG TAT TAC GCT CAA CTT CAG AAT CTC ACT AAA	534										
Glu Lys Glu Lys Asp Trp Tyr Tyr Ala Gln Leu Gln Asn Leu Thr Lys											
	155	160	165								
AGA ATA GAT AGT CTT CCT TTA ACT GAA AAT TTT TCG TTA CAA ACA GAT	582										
Arg Ile Asp Ser Leu Pro Leu Thr Glu Asn Phe Ser Leu Gln Thr Asp											
	170	175	180								
TTG ACC AGA AGG CAA TTG GAA TAT GAA GAA AGG CAA ATC AGA GTT GCG	630										
Leu Thr Arg Arg Gln Leu Glu Tyr Glu Ala Arg Gln Ile Arg Val Ala											
	185	190	195								
ATG GAA GAA CAA CTA GGT ACC TGC CAG GAT ATG GAA AAA CGA GCA CAG	678										
Met Glu Glu Gln Leu Gly Thr Cys Gln Asp Met Glu Lys Arg Ala Gln											
	200	205	210								
CGA AGA ATA GCC AGA ATT CAG CAA ATC GAA AAG GAC ATA CTT CGT ATA	726										
Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu Lys Asp Ile Leu Arg Ile											
	220	225	230								
CGA CAG CTT TTA CAG TCC CAA GCA ACA GAA GCA GAG AGG TCA TCT CAG	774										
Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu Ala Glu Arg Ser Ser Gln											
	235	240	245								
AAC AAG CAT GAA ACC GGC TCA CAT GAT GCT GAG CGG CAG AAT GAA GGT	822										
Asn Lys His Glu Thr Gly Ser His Asp Ala Glu Arg Gln Asn Glu Gly											
	250	255	260								
CAA GGA GTG GGA GAA ATC AAC ATG GCA ACT TCT GGT AAT GGT CAG GGT	870										
Gln Gly Val Gly Glu Ile Asn Met Ala Thr Ser Gly Asn Gly Gln Gly											
	265	270	275								
TCA ACT ACA CGA ATG GAC CAT GAA ACA GCC AGT GTT TTG AGT TCT AGT	918										
Ser Thr Thr Arg Met Asp His Glu Thr Ala Ser Val Leu Ser Ser Ser											
	280	285	290								

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AGC	ACA	CAC	TCT	GCA	CCT	CGA	AGG	CTG	ACA	AGT	CAT	CTG	GGA	ACC	AAG	966
Ser	Thr	His	Ser	Ala	Pro	Arg	Arg	Leu	Thr	Ser	His	Leu	Gly	Thr	Lys	
				300					305					310		
GTG	GAA	ATG	GTG	TAT	TCA	TTG	TTG	TCA	ATG	CTT	GGT	ACT	CAT	GAT	AAG	1014
Val	Glu	Met	Val	Tyr	Ser	Leu	Leu	Ser	Met	Leu	Gly	Thr	His	Asp	Lys	
			315					320					325			
GAT	GAT	ATG	TCG	CGA	ACT	TTG	CTA	GCT	ATG	TCT	AGC	TCC	CAA	GAC	AGC	1062
Asp	Asp		Ser	Arg	Thr	Leu	Leu	Ala	Met	Ser	Ser	Ser	Gln	Asp	Ser	
		330					335					340				
TGT	ATA	TCC	ATG	CGA	CAG	TCT	GGA	TGT	CTT	CCT	CTC	CTC	ATC	CAG	CTT	1110
Cys	Ile	Ser	Met	Arg	Gln	Ser	Gly	Cys	Leu	Pro	Leu	Leu	Ile	Gln	Leu	
	345					350					355					
TTA	CAT	GGC	AAT	GAC	AAA	GAC	TCT	GTA	TTG	TTG	GGA	AAT	TCC	CGG	GGC	1158
Leu	His	Gly	Asn	Asp	Lys	Asp	Ser	Val	Leu	Leu	Gly	Asn	Ser	Arg	Gly	
	360			365				370							375	
AGT	AAA	GAG	GCT	CGG	GCC	AGG	GCC	AGT	GCA	GCA	CTC	CAC	AAC	ATC	ATT	1206
Ser	Lys	Glu	Ala	Arg	Ala	Arg	Ala	Ser	Ala	Ala	Leu	His	Asn	Ile	Ile	
				380					385					390		
CAC	TCA	CAG	CCT	GAT	GAC	AAG	AGA	GGC	AGG	CGT	GAA	ATC	CGA	GTC	CTT	1254
His	Ser	Gln	Pro	Asp	Asp	Lys	Arg	Gly	Arg	Arg	Glu	Ile	Arg	Val	Leu	
			395					400					405			
CAT	CTT	TTG	GAA	CAG	ATA	CGC	GCT	TAC	TGT	GAA	ACC	TGT	TGG	GAG	TGG	1302
His	Leu	Leu	Glu	Gln	Ile	Arg	Ala	Tyr	Cys	Glu	Thr	Cys	Trp	Glu	Trp	
			410				415					420				
CAG	GAA	GCT	CAT	GAA	CCA	GGC	ATG	GAC	CAG	GAC	AAA	AAT	CCA	ATG	CCA	1350
Gln	Glu	Ala	His	Glu	Pro	Gly	Met	Asp	Gln	Asp	Lys	Asn	Pro	Met	Pro	
	425					430					435					
GCT	CCT	GTT	GAA	CAT	CAG	ATC	TGT	CCT	GCT	GTG	TGT	GTT	CTA	ATG	AAA	1398
Ala	Pro	Val	Glu	His	Gln	Ile	Cys	Pro	Ala	Val	Cys	Val	Leu	Met	Lys	
	440				445				450						455	
CTT	TCA	TTT	GAT	GAA	GAG	CAT	AGA	CAT	GCA	ATG	AAT	GAA	CTA	GGG	GGA	1446
Leu	Ser	Phe	Asp	Glu	Glu	His	Arg	His	Ala	Met	Asn	Glu	Leu	Gly	Gly	
			460					465						470		
CTA	CAG	GCC	ATT	GCA	GAA	TTA	TTG	CAA	GTG	GAC	TGT	GAA	ATG	TAT	GGG	1494
Leu	Gln	Ala	Ile	Ala	Glu	Leu	Leu	Gln	Val	Asp	Cys	Glu	Met	Tyr	Gly	
			475				480						485			
CTT	ACT	AAT	GAC	CAC	TAC	AGT	ATT	ACA	CTA	AGA	CGA	TAT	GCT	GGA	ATG	1542
Leu	Thr	Asn	Asp	His	Tyr	Ser	Ile	Thr	Leu	Arg	Arg	Tyr	Ala	Gly	Met	
		490					495					500				
GCT	TTG	ACA	AAC	TTG	ACT	TTT	GGA	GAT	GTA	GCC	AAC	AAG	GCT	ACG	CTA	1590
Ala	Leu	Thr	Asn	Leu	Thr	Phe	Gly	Asp	Val	Ala	Asn	Lys	Ala	Thr	Leu	
	505					510				515						
TGC	TCT	ATG	AAA	GGC	TGC	ATG	AGA	GCA	CTT	GTG	GCC	CAA	CTA	AAA	TCT	1638
Cys	Ser	Met	Lys	Gly	Cys	Met	Arg	Ala	Leu	Val	Ala	Gln	Leu	Lys	Ser	
	520				525					530					535	
GAA	AGT	GAA	GAC	TTA	CAG	CAG	GTT	ATT	GCA	AGT	GTT	TTG	AGG	AAT	TTG	1686
Glu	Ser	Glu	Asp	Leu	Gln	Gln	Val	Ile	Ala	Ser	Val	Leu	Arg	Asn	Leu	
			540						545					550		
TCT	TGG	CGA	GCA	GAT	GTA	AAT	AGT	AAA	AAG	ACG	TTG	CGA	GAA	GTT	GGA	1734
Ser	Trp	Arg	Ala	Asp	Val	Asn	Ser	Lys	Lys	Thr	Leu	Arg	Glu	Val	Gly	
			555					560					565			
AGT	GTG	AAA	GCA	TTG	ATG	GAA	TGT	GCT	TTA	GAA	GTT	AAA	AAG	GAA	TCA	1782
Ser	Val	Lys	Ala	Leu	Met	Glu	Cys	Ala	Leu	Glu	Val	Lys	Lys	Glu	Ser	
		570					575					580				
ACC	CTC	AAA	AGC	GTA	TTG	AGT	GCC	TTA	TGG	AAT	TTG	TCA	GCA	CAT	TGC	1830
Thr	Leu	Lys	Ser	Val	Leu	Ser	Ala	Leu	Trp	Asn	Leu	Ser	Ala	His	Cys	
	585					590					595					
ACT	GAG	AAT	AAA	GCT	GAT	ATA	TGT	GCT	GTA	GAT	GGT	GCA	CTT	GCA	TTT	1878
Thr	Glu	Asn	Lys	Ala	Asp	Ile	Cys	Ala	Val	Asp	Gly	Ala	Leu	Ala	Phe	
	600				605					610					615	

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TTG	GTT	GGC	ACT	CTT	ACT	TAC	COG	AGC	CAG	ACA	AAC	ACT	TTA	GCC	ATT	1926
Leu	Val	Gly	Thr	Leu	Thr	Tyr	Arg	Ser	Gln	Thr	Asn	Thr	Leu	Ala	Ile	
				620					625					630		
ATT	GAA	AGT	GGA	GGT	GGG	ATA	TTA	CGG	AAT	GTG	TCC	AGC	TTG	ATA	GCT	1974
Ile	Glu	Ser	Gly	Gly	Gly	Ile	Leu	Arg	Asn	Val	Ser	Ser	Leu	Ile	Ala	
			635					640					645			
ACA	AAT	GAG	GAC	CAC	AGG	CAA	ATC	CTA	AGA	GAG	AAC	AAC	TGT	CTA	CAA	2022
Thr	Asn	Glu	Asp	His	Arg	Gln	Ile	Leu	Arg	Glu	Asn	Asn	Cys	Leu	Gln	
		650					655					660				
ACT	TTA	TTA	CAA	CAC	TTA	AAA	TCT	CAT	AGT	TTG	ACA	ATA	GTC	AGT	AAT	2070
Thr	Leu	Leu	Gln	His	Leu	Lys	Ser	His	Ser	Leu	Thr	Ile	Val	Ser	Asn	
	665					670					675					
GCA	TGT	GGA	ACT	TTG	TGG	AAT	CTC	TCA	GCA	AGA	AAT	CCT	AAA	GAC	CAG	2118
Ala	Cys	Gly	Thr	Leu	Trp	Asn	Leu	Ser	Ala	Arg	Asn	Pro	Lys	Asp	Gln	
	680				685					690					695	
GAA	GCA	TTA	TGG	GAC	ATG	GGG	GCA	GTT	AGC	ATG	CTC	AAG	AAC	CTC	ATT	2166
Glu	Ala	Leu	Trp	Asp	Met	Gly	Ala	Val	Ser	Met	Leu	Lys	Asn	Leu	Ile	
			700						705					710		
CAT	TCA	AAG	CAC	AAA	ATG	ATT	GCT	ATG	GGA	AGT	GCT	GCA	GCT	TTA	AGG	2214
His	Ser	Lys	His	Lys	Met	Ile	Ala	Met	Gly	Ser	Ala	Ala	Ala	Leu	Arg	
			715					720					725			
AAT	CTC	ATG	GCA	AAT	AGG	CCT	GCG	AAG	TAC	AAG	GAT	GCC	AAT	ATT	ATG	2262
Asn	Leu	Met	Ala	Asn	Arg	Pro	Ala	Lys	Tyr	Lys	Asp	Ala	Asn	Ile	Met	
		730					735					740				
TCT	CCT	GGC	TCA	AGC	TTG	CCA	TCT	CTT	CAT	GTT	AGG	AAA	CAA	AAA	GCC	2310
Ser	Pro	Gly	Ser	Ser	Leu	Pro	Ser	Leu	His	Val	Arg	Lys	Gln	Lys	Ala	
		745				750					755					
CTA	GAA	GCA	GAA	TTA	GAT	GCT	CAG	CAC	TTA	TCA	GAA	ACT	TTT	GAC	AAT	2358
Leu	Glu	Ala	Glu	Leu	Asp	Ala	Gln	His	Leu	Ser	Glu	Thr	Phe	Asp	Asn	
					765					770					775	
ATA	GAC	AAT	TTA	AGT	CCC	AAG	GCA	TCT	CAT	CGT	AGT	AAG	CAG	AGA	CAC	2406
Ile	Asp	Asn	Leu	Ser	Pro	Lys	Ala	Ser	His	Arg	Ser	Lys	Gln	Arg	His	
				780					785					790		
AAG	CAA	AGT	CTC	TAT	GGT	GAT	TAT	GTT	TTT	GAC	ACC	AAT	CGA	CAT	GAT	2454
Lys	Gln	Ser	Leu	Tyr	Gly	Asp	Tyr	Val	Phe	Asp	Thr	Asn	Arg	His	Asp	
			795					800					805			
GAT	AAT	AGG	TCA	GAC	AAT	TTT	AAT	ACT	GGC	AAC	ATG	ACT	GTC	CTT	TCA	2502
Asp	Asn	Arg	Ser	Asp	Asn	Phe	Asn	Thr	Gly	Asn	Met	Thr	Val	Leu	Ser	
		810					815					820				
CCA	TAT	TTG	AAT	ACT	ACA	GTG	TTA	CCC	AGC	TCC	TCT	TCA	TCA	AGA	GGA	2550
Pro	Tyr	Leu	Asn	Thr	Thr	Val	Leu	Pro	Ser	Ser	Ser	Ser	Ser	Arg	Gly	
		825				830					835					
AGC	TTA	GAT	AGT	TCT	CGT	TCT	GAA	AAA	GAT	AGA	AGT	TTG	GAG	AGA	GAA	2598
Ser	Leu	Asp	Ser	Ser	Ser	Ser	Glu	Lys	Asp	Arg	Ser	Leu	Glu	Arg	Glu	
		840			845					850					855	
CGC	GGA	ATT	GGT	CTA	GGC	AAC	TAC	CAT	CCA	GCA	ACA	GAA	AAT	CCA	GGA	2646
Arg	Gly	Ile	Gly	Leu	Gly	Asn	Tyr	His	Pro	Ala	Thr	Glu	Asn	Pro	Gly	
				860					865					870		
ACT	TCT	TCA	AAG	CGA	GGT	TTG	CAG	ATC	TCC	ACC	ACT	GCA	GCC	CAG	ATT	2694
Thr	Ser	Ser	Lys	Arg	Gly	Leu	Gln	Ile	Ser	Thr	Thr	Ala	Ala	Gln	Ile	
			875					880					885			
GCC	AAA	GTC	ATG	GAA	GAA	GTG	TCA	GCC	ATT	CAT	ACC	TCT	CAG	GAA	GAC	2742
Ala	Lys	Val	Met	Glu	Glu	Val	Ser	Ala	Ile	His	Thr	Ser	Gln	Glu	Asp	
		890					895					900				
AGA	AGT	TCT	GGG	TCT	ACC	ACT	GAA	TTA	CAT	TGT	GTG	ACA	GAT	GAG	AGA	2790
Arg	Ser	Ser	Gly	Ser	Thr	Thr	Glu	Leu	His	Cys	Val	Thr	Asp	Glu	Arg	
		905				910					915					
AAT	GCA	CTT	AGA	AGA	AGC	TCT	GCT	GCC	CAT	ACA	CAT	TCA	AAC	ACT	TAC	2838
Asn	Ala	Leu	Arg	Arg	Ser	Ser	Ala	Ala	His	Thr	His	Ser	Asn	Thr	Tyr	
		920			925					930					935	

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AAT	TTC	ACT	AAG	TCG	GAA	AAT	TCA	AAT	AGG	ACA	TGT	TCT	ATG	CCT	TAT	2886
Asn	Phe	Thr	Lys	Ser	Glu	Asn	Ser	Asn	Arg	Thr	Cys	Ser	Met	Pro	Tyr	
				940					945					950		
GCC	AAA	TTA	GAA	TAC	AAG	AGA	TCT	TCA	AAT	GAT	AGT	TTA	AAT	AGT	GTC	2934
Ala	Lys	Leu	Glu	Tyr	Lys	Arg	Ser	Ser	Asn	Asp	Ser	Leu	Asn	Ser	Val	
			955					960						965		
AGT	AGT	AAT	GAT	GGT	TAT	GGT	AAA	AGA	GGT	CAA	ATG	AAA	CCC	TCG	ATT	2982
Ser	Ser	Asn	Asp	Gly	Tyr	Gly	Lys	Arg	Gly	Gln	Met	Lys	Pro	Ser	Ile	
		970					975					980				
GAA	TCC	TAT	TCT	GAA	GAT	GAT	GAA	AGT	AAG	TTT	TGC	AGT	TAT	GGT	CAA	3030
Glu	Ser	Tyr	Ser	Glu	Asp	Asp	Glu	Ser	Lys	Phe	Cys	Ser	Tyr	Gly	Gln	
	985					990					995					
TAC	CCA	GCC	GAC	CTA	GCC	CAT	AAA	ATA	CAT	AGT	GCA	AAT	CAT	ATG	GAT	3078
Tyr	Pro	Ala	Asp	Leu	Ala	His	Lys	Ile	His	Ser	Ala	Asn	His	Met	Asp	
1000					1005					1010					1015	
GAT	AAT	GAT	GGA	GAA	CTA	GAT	ACA	CCA	ATA	AAT	TAT	AGT	CTT	AAA	TAT	3126
Asp	Asn	Asp	Gly	Glu	Leu	Asp	Thr	Pro	Ile	Asn	Tyr	Ser	Leu	Lys	Tyr	
			1020						1025					1030		
TCA	GAT	GAG	CAG	TTG	AAC	TCT	GGA	AGG	CAA	AGT	CCT	TCA	CAG	AAT	GAA	3174
Ser	Asp	Glu	Gln	Leu	Asn	Ser	Gly	Arg	Gln	Ser	Pro	Ser	Gln	Asn	Glu	
			1035					1040					1045			
AGA	TGG	GCA	AGA	CCC	AAA	CAC	ATA	ATA	GAA	GAT	GAA	ATA	AAA	CAA	AGT	3222
Arg	Trp	Ala	Arg	Pro	Lys	His	Ile	Ile	Glu	Asp	Glu	Ile	Lys	Gln	Ser	
	1050						1055					1060				
GAG	CAA	AGA	CAA	TCA	AGG	AAT	CAA	AGT	ACA	ACT	TAT	CCT	GTT	TAT	ACT	3270
Glu	Gln	Arg	Gln	Ser	Arg	Asn	Gln	Ser	Thr	Thr	Tyr	Pro	Val	Tyr	Thr	
	1065					1070					1075					
GAG	AGC	ACT	GAT	GAT	AAA	CAC	CTC	AAG	TTC	CAA	CCA	CAT	TTT	GGA	CAG	3318
Glu	Ser	Thr	Asp	Asp	Lys	His	Leu	Lys	Phe	Gln	Pro	His	Phe	Gly	Gln	
1080					1085					1090					1095	
CAG	GAA	TGT	GTT	TCT	CCA	TAC	AGG	TCA	CGG	GGA	GCC	AAT	GGT	TCA	GAA	3366
Gln	Glu	Cys	Val	Ser	Pro	Tyr	Arg	Ser	Arg	Gly	Ala	Asn	Gly	Ser	Glu	
				1100					1105				1110			
ACA	AAT	CGA	GTG	GGT	TCT	AAT	CAT	GGA	ATT	AAT	CAA	AAT	GTA	AGC	CAG	3414
Thr	Asn	Arg	Val	Gly	Ser	Asn	His	Gly	Ile	Asn	Gln	Asn	Val	Ser	Gln	
			1115					1120					1125			
TCT	TTG	TGT	CAA	GAA	GAT	GAC	TAT	GAA	GAT	GAT	AAG	CCT	ACC	AAT	TAT	3462
Ser	Leu	Cys	Gln	Glu	Asp	Asp	Tyr	Glu	Asp	Asp	Lys	Pro	Thr	Asn	Tyr	
		1130					1135					1140				
AGT	GAA	COT	TAC	TCT	GAA	GAA	GAA	CAG	CAT	GAA	GAA	GAA	GAG	AGA	CCA	3510
Ser	Glu	Arg	Tyr	Ser	Glu	Glu	Glu	Gln	His	Glu	Glu	Glu	Glu	Arg	Pro	
	1145				1150					1155						
ACA	AAT	TAT	AGC	ATA	AAA	TAT	AAT	GAA	GAG	AAA	CCT	CAT	GTG	GAT	CAG	3558
Thr	Asn	Tyr	Ser	Ile	Lys	Tyr	Asn	Glu	Glu	Lys	Arg	His	Val	Asp	Gln	
1160				1165						1170					1175	
CCT	ATT	GAT	TAT	AGT	TTA	AAA	TAT	GCC	ACA	GAT	ATT	CCT	TCA	TCA	CAG	3606
Pro	Ile	Asp	Tyr	Ser	Leu	Lys	Tyr	Ala	Thr	Asp	Ile	Pro	Ser	Ser	Gln	
				1180					1185					1190		
AAA	CAG	TCA	TTT	TCA	TTC	TCA	AAG	AGT	TCA	TCT	GGA	CAA	AGC	AGT	AAA	3654
Lys	Gln	Ser	Phe	Ser	Phe	Ser	Lys	Ser	Ser	Ser	Gly	Gln	Ser	Ser	Lys	
			1195					1200					1205			
ACC	GAA	CAT	ATG	TCT	TCA	AGC	AGT	GAG	AAT	ACG	TCC	ACA	CCT	TCA	TCT	3702
Thr	Glu	His	Met	Ser	Ser	Ser	Ser	Glu	Asn	Thr	Ser	Thr	Pro	Ser	Ser	
		1210					1215					1220				
AAT	GCC	AAG	AGG	CAG	AAT	CAG	CTC	CAT	CCA	AGT	TCT	GCA	CAG	AGT	AGA	3750
Asn	Ala	Lys	Arg	Gln	Asn	Gln	Leu	His	Pro	Ser	Ser	Ala	Gln	Ser	Arg	
	1225					1230						1235				
AGT	GGT	CAG	CCT	CAA	AAG	GCT	GCC	ACT	TGC	AAA	GTT	TCT	TCT	ATT	AAC	3798
Ser	Gly	Gln	Pro	Gln	Lys	Ala	Ala	Thr	Cys	Lys	Val	Ser	Ser	Ile	Asn	
1240					1245					1250					1255	

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CAA	GAA	ACA	ATA	CAG	ACT	TAT	TGT	GTA	GAA	GAT	ACT	CCA	ATA	TGT	TTT	3846
Gln	Glu	Thr	Ile	Gln	Thr	Tyr	Cys	Val	Glu	Asp	Thr	Pro	Ile	Cys	Phe	
				1260					1265					1270		
TCA	AGA	TGT	AGT	TCA	TTA	TCA	TCT	TTG	TCA	TCA	GCT	GAA	GAT	GAA	ATA	3894
Ser	Arg	Cys	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Ser	Ala	Glu	Asp	Glu	Ile	
			1275					1280					1285			
GGA	TGT	AAT	CAG	ACG	ACA	CAG	GAA	GCA	GAT	TCT	GCT	AAT	ACC	CTG	CAA	3942
Gly	Cys	Asn	Gln	Thr	Thr	Gln	Glu	Ala	Asp	Ser	Ala	Asn	Thr	Leu	Gln	
		1290					1295					1300				
ATA	GCA	GAA	ATA	AAA	GGA	AAG	ATT	GGA	ACT	AGG	TCA	GCT	GAA	GAT	CCT	3990
Ile	Ala	Glu	Ile	Lys	Gly	Lys	Ile	Gly	Thr	Arg	Ser	Ala	Glu	Asp	Pro	
	1305					1310				1315						
GTG	AGC	GAA	GTT	CCA	GCA	GTG	TCA	CAG	CAC	CCT	AGA	ACC	AAA	TCC	AGC	4038
Val	Ser	Glu	Val	Pro	Ala	Val	Ser	Gln	His	Pro	Arg	Thr	Lys	Ser	Ser	
	1320				1325					1330					1335	
AGA	CTG	CAG	GGT	TCT	AGT	TTA	TCT	TCA	GAA	TCA	GCC	AGG	CAC	AAA	GCT	4086
Arg	Leu	Gln	Gly	Ser	Ser	Leu	Ser	Ser	Glu	Ser	Ala	Arg	His	Lys	Ala	
			1340						1345					1350		
GTT	GAA	TTT	CCT	TCA	GGA	GCG	AAA	TCT	CCC	TCC	AAA	AGT	GGT	GCT	CAG	4134
Val	Glu	Phe	Pro	Ser	Gly	Ala	Lys	Ser	Pro	Ser	Lys	Ser	Gly	Ala	Gln	
			1355					1360					1365			
ACA	CCC	AAA	AGT	CCA	CCT	GAA	CAC	TAT	GTT	CAG	GAG	ACC	CCA	CTC	ATG	4182
Thr	Pro	Lys	Ser	Pro	Pro	Glu	His	Tyr	Val	Gln	Glu	Thr	Pro	Leu	Met	
		1370					1375					1380				
TTT	AGC	AGA	TGT	ACT	TCT	GTC	AGT	TCA	CTT	GAT	AGT	TTT	GAG	AGT	CGT	4230
Phe	Ser	Arg	Cys	Thr	Ser	Val	Ser	Ser	Leu	Asp	Ser	Phe	Glu	Ser	Arg	
	1385					1390					1395					
TCG	ATT	GCC	AGC	TCC	GTT	CAG	AGT	GAA	CCA	TGC	AGT	GGA	ATG	GTA	AGT	4278
Ser	Ile	Ala	Ser	Ser	Val	Gln	Ser	Glu	Pro	Cys	Ser	Gly	Met	Val	Ser	
	1400				1405					1410					1415	
GGC	ATT	ATA	AGC	CCC	AGT	GAT	CTT	CCA	GAT	AGC	CCT	GGA	CAA	ACC	ATG	4326
Gly	Ile	Ile	Ser	Pro	Ser	Asp	Leu	Pro	Asp	Ser	Pro	Gly	Gln	Thr	Met	
			1420						1425					1430		
CCA	CCA	AGC	AGA	AGT	AAA	ACA	CCT	CCA	CCA	CCT	CCT	CAA	ACA	GCT	CAA	4374
Pro	Pro	Ser	Arg	Ser	Lys	Thr	Pro	Pro	Pro	Pro	Pro	Gln	Thr	Ala	Gln	
			1435					1440					1445			
ACC	AAG	CGA	GAA	GTA	CCT	AAA	AAT	AAA	GCA	CCT	ACT	GCT	GAA	AAG	AGA	4422
Thr	Lys	Arg	Glu	Val	Pro	Lys	Asn	Lys	Ala	Pro	Thr	Ala	Glu	Lys	Arg	
		1450					1455					1460				
GAG	AGT	GGA	CCT	AAG	CAA	GCT	GCA	GTA	AAT	GCT	GCA	GTT	CAG	AGG	GTC	4470
Glu	Ser	Gly	Pro	Lys	Gln	Ala	Ala	Val	Asn	Ala	Ala	Val	Gln	Arg	Val	
	1465					1470					1475					
CAG	GTT	CTT	CCA	GAT	GCT	GAT	ACT	TTA	TTA	CAT	TTT	GCC	ACA	GAA	AGT	4518
Gln	Val	Leu	Pro	Asp	Ala	Asp	Thr	Leu	Leu	His	Phe	Ala	Thr	Glu	Ser	
	1480				1485					1490					1495	
ACT	CCA	GAT	GGA	TTT	TCT	TGT	TCA	TCC	AGC	CTG	AGT	GCT	CTG	AGC	CTC	4566
Thr	Pro	Asp	Gly	Phe	Ser	Cys	Ser	Ser	Ser	Leu	Ser	Ala	Leu	Ser	Leu	
			1500						1505					1510		
GAT	GAG	CCA	TTT	ATA	CAG	AAA	GAT	GTG	GAA	TTA	AGA	ATA	ATG	CCT	CCA	4614
Asp	Glu	Pro	Phe	Ile	Gln	Lys	Asp	Val	Glu	Leu	Arg	Ile	Met	Pro	Pro	
			1515					1520					1525			
GTT	CAG	GAA	AAT	GAC	AAT	GGG	AAT	GAA	ACA	GAA	TCA	GAG	CAG	CCT	AAA	4662
Val	Gln	Glu	Asn	Asp	Asn	Gly	Asn	Glu	Thr	Glu	Ser	Glu	Gln	Pro	Lys	
		1530					1535					1540				
GAA	TCA	AAT	GAA	AAC	CAA	GAG	AAA	GAG	GCA	GAA	AAA	ACT	ATT	GAT	TCT	4710
Glu	Ser	Asn	Glu	Asn	Gln	Glu	Lys	Glu	Ala	Glu	Lys	Thr	Ile	Asp	Ser	
	1545					1550					1555					
GAA	AAG	GAC	CTA	TTA	GAT	GAT	TCA	GAT	GAT	GAT	GAT	ATT	GAA	ATA	CTA	4758
Glu	Lys	Asp	Leu	Leu	Asp	Asp	Ser	Asp	Asp	Asp	Asp	Ile	Glu	Ile	Leu	
	1560				1565				1570					1575		

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GAA	GAA	TGT	ATT	ATT	TCT	GCC	ATG	CCA	ACA	AAG	TCA	TCA	CGT	AAA	GGC	4806
Glu	Glu	Cys	Ile	Ile	Ser	Ala	Met	Pro	Thr	Lys	Ser	Ser	Arg	Lys	Gly	
			1580						1585					1590		
AAA	AAG	CCA	GCC	CAG	ACT	GCT	TCA	AAA	TTA	CCT	CCA	CCT	GTG	GCA	AGG	4854
Lys	Lys	Pro	Ala	Gln	Thr	Ala	Ser	Lys	Leu	Pro	Pro	Pro	Val	Ala	Arg	
			1595					1600					1605			
AAA	CCA	AGT	CAG	CTG	CCT	GTG	TAC	AAA	CTT	CTA	CCA	TCA	CAA	AAC	AGG	4902
Lys	Pro	Ser	Gln	Leu	Pro	Val	Tyr	Lys	Leu	Leu	Pro	Ser	Gln	Asn	Arg	
		1610					1615					1620				
TTG	CAA	CCC	CAA	AAG	CAT	GTT	AGT	TTT	ACA	CCG	GGG	GAT	GAT	ATG	CCA	4950
Leu	Gln	Pro	Gln	Lys	His	Val	Ser	Phe	Thr	Pro	Gly	Asp	Asp	Met	Pro	
	1625					1630					1635					
CGG	GTG	TAT	TGT	GTT	GAA	GGG	ACA	CCT	ATA	AAC	TTT	TCC	ACA	GCT	ACA	4998
Arg	Val	Tyr	Cys	Val	Glu	Gly	Thr	Pro	Ile	Asn	Phe	Ser	Thr	Ala	Thr	
	1640				1645				1650					1655		
TCT	CTA	AGT	GAT	CTA	ACA	ATC	GAA	TCC	CCT	CCA	AAT	GAG	TTA	GCT	GCT	5046
Ser	Leu	Ser	Asp	Leu	Thr	Ile	Glu	Ser	Pro	Pro	Asn	Glu	Leu	Ala	Ala	
				1660					1665					1670		
GGA	GAA	GGA	GTT	AGA	GGA	GGA	GCA	CAG	TCA	GGT	GAA	TTT	GAA	AAA	CGA	5094
Gly	Glu	Gly	Val	Arg	Gly	Gly	Ala	Gln	Ser	Gly	Glu	Phe	Glu	Lys	Arg	
			1675					1680					1685			
GAT	ACC	ATT	CCT	ACA	GAA	GGC	AGA	AGT	ACA	GAT	GAG	GCT	CAA	GGA	GGA	5142
Asp	Thr	Ile	Pro	Thr	Glu	Gly	Arg	Ser	Thr	Asp	Glu	Ala	Gln	Gly	Gly	
		1690					1695					1700				
AAA	ACC	TCA	TCT	GTA	ACC	ATA	CCT	GAA	TTG	GAT	GAC	AAT	AAA	GCA	GAG	5190
Lys	Thr	Ser	Ser	Val	Thr	Ile	Pro	Glu	Leu	Asp	Asp	Asn	Lys	Ala	Glu	
	1705					1710					1715					
GAA	GGT	GAT	ATT	CTT	GCA	GAA	TGC	ATT	AAT	TCT	GCT	ATG	CCC	AAA	GGG	5238
Glu	Gly	Asp	Ile	Leu	Ala	Glu	Cys	Ile	Asn	Ser	Ala	Met	Pro	Lys	Gly	
	1720				1725				1730					1735		
AAA	AGT	CAC	AAG	CCT	TTC	CGT	GTG	AAA	AAG	ATA	ATG	GAC	CAG	GTC	CAG	5286
Lys	Ser	His	Lys	Pro	Phe	Arg	Val	Lys	Lys	Ile	Met	Asp	Gln	Val	Gln	
				1740					1745					1750		
CAA	GCA	TCT	GCG	TCG	TCT	TCT	GCA	CCC	AAA	AAA	AAT	CAG	TTA	GAT	GGT	5334
Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro	Ala	Lys	Asn	Gln	Leu	Asp	Gly	
			1755					1760					1765			
AAG	AAA	AAG	AAA	CCA	ACT	TCA	CCA	GTA	AAA	CCT	ATA	CCA	CAA	AAT	ACT	5382
Lys	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val	Lys	Pro	Ile	Pro	Gln	Asn	Thr	
			1770				1775					1780				
GAA	TAT	AGG	ACA	CGT	GTA	AGA	AAA	AAT	GCA	GAC	TCA	AAA	AAT	AAT	TTA	5430
Glu	Tyr	Arg	Thr	Arg	Val	Arg	Lys	Asn	Ala	Asp	Ser	Lys	Asn	Asn	Leu	
	1785				1790						1795					
AAT	GCT	GAG	AGA	GTT	TTC	TCA	GAC	AAG	AAA	GAT	TCA	AAG	AAA	CAG	AAT	5478
Asn	Ala	Glu	Arg	Val	Phe	Ser	Asp	Asn	Lys	Asp	Ser	Lys	Lys	Gln	Asn	
	1800				1805					1810				1815		
TTG	AAA	AAT	AAT	TCC	AAG	GAC	TTC	AAT	GAT	AAG	CTC	CCA	AAT	AAT	GAA	5526
Leu	Lys	Asn	Asn	Ser	Lys	Asp	Phe	Asn	Asp	Lys	Leu	Pro	Asn	Asn	Glu	
				1820					1825					1830		
GAT	AGA	GTC	AGA	GGA	AGT	TTT	GCT	TTT	GAT	TCA	CCT	CAT	CAT	TAC	ACG	5574
Asp	Arg	Val	Arg	Gly	Ser	Phe	Ala	Phe	Asp	Ser	Pro	His	His	Tyr	Thr	
			1835					1840					1845			
CCT	ATT	GAA	GGA	ACT	CCT	TAC	TGT	TTT	TCA	CGA	AAT	GAT	TCT	TTG	AGT	5622
Pro	Ile	Glu	Gly	Thr	Pro	Tyr	Cys	Phe	Ser	Arg	Asn	Asp	Ser	Leu	Ser	
		1850					1855						1860			
TCT	CTA	GAT	TTT	GAT	GAT	GAT	GAT	GTT	GAC	CTT	TCC	AGG	GAA	AAG	GCT	5670
Ser	Leu	Asp	Phe	Asp	Asp	Asp	Asp	Val	Asp	Leu	Ser	Arg	Glu	Lys	Ala	
		1865				1870					1875					
GAA	TTA	AGA	AAG	GCA	AAA	GAA	AAT	AAG	GAA	TCA	GAG	GCT	AAA	GTT	ACC	5718
Glu	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Lys	Glu	Ser	Glu	Ala	Lys	Val	Thr	
	1880				1885					1890				1895		

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AGC	CAC	ACA	GAA	CTA	ACC	TCC	AAC	CAA	CAA	TCA	GCT	AAT	AAG	ACA	CAA	5766
Ser	His	Thr	Glu	Leu	Thr	Ser	Asn	Gln	Gln	Ser	Ala	Asn	Lys	Thr	Gln	
				1900												
GCT	ATT	GCA	AAG	CAG	CCA	ATA	AAT	CGA	GGT	CAG	CCT	AAA	CCC	ATA	CTT	5814
Ala	Ile	Ala	Lys	Gln	Pro	Ile	Asn	Arg	Gly	Gln	Pro	Lys	Pro	Ile	Leu	
			1915					1920					1925			
CAG	AAA	CAA	TCC	ACT	TTT	CCC	CAG	TCA	TCC	AAA	GAC	ATA	CCA	GAC	AGA	5862
Gln	Lys	Gln	Ser	Thr	Phe	Pro	Gln	Ser	Ser	Lys	Asp	Ile	Pro	Asp	Arg	
			1930				1935					1940				
GGG	GCA	GCA	ACT	GAT	GAA	AAG	TTA	CAG	AAT	TTT	GCT	ATT	GAA	AAT	ACT	5910
Gly	Ala	Ala	Thr	Asp	Glu	Lys	Leu	Gln	Asn	Phe	Ala	Ile	Glu	Asn	Thr	
			1945			1950					1955					
CCA	GTT	TGC	TTT	TCT	CAT	AAT	TCC	TCT	CTG	AGT	TCT	CTC	AGT	GAC	ATT	5958
Pro	Val	Cys	Phe	Ser	His	Asn	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Asp	Ile	
					1965					1970					1975	
GAC	CAA	GAA	AAC	AAC	AAT	AAA	GAA	AAT	GAA	CCT	ATC	AAA	GAG	ACT	GAG	6006
Asp	Gln	Glu	Asn	Asn	Asn	Lys	Glu	Asn	Glu	Pro	Ile	Lys	Glu	Thr	Glu	
				1980						1985					1990	
CCC	CCT	GAC	TCA	CAG	GGA	GAA	CCA	AGT	AAA	CCT	CAA	GCA	TCA	GGC	TAT	6054
Pro	Pro	Asp	Ser	Gln	Gly	Glu	Pro	Ser	Lys	Pro	Gln	Ala	Ser	Gly	Tyr	
				1995				2000					2005			
GCT	CCT	AAA	TCA	TTT	CAT	GTT	GAA	GAT	ACC	CCA	GTT	TGT	TTC	TCA	AGA	6102
Ala	Pro	Lys	Ser	Phe	His	Val	Glu	Asp	Thr	Pro	Val	Cys	Phe	Ser	Arg	
			2010				2015					2020				
AAC	AGT	TCT	CTC	AGT	TCT	CTT	AGT	ATT	GAC	TCT	GAA	GAT	GAC	CTG	TTG	6150
Asn	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Ile	Asp	Ser	Glu	Asp	Asp	Leu	Leu	
			2025			2030					2035					
CAG	GAA	TGT	ATA	AGC	TCC	GCA	ATG	CCA	AAA	AAG	AAA	AAG	CCT	TCA	AGA	6198
Gln	Glu	Cys	Ile	Ser	Ser	Ala	Met	Pro	Lys	Lys	Lys	Lys	Pro	Ser	Arg	
			2040			2045				2050					2055	
CTC	AAG	GGT	GAT	AAT	GAA	AAA	CAT	AGT	CCC	AGA	AAT	ATG	GGT	GGC	ATA	6246
Leu	Lys	Gly	Asp	Asn	Glu	Lys	His	Ser	Pro	Arg	Asn	Met	Gly	Gly	Ile	
				2060					2065						2070	
TTA	GGT	GAA	GAT	CTG	ACA	CTT	GAT	TTG	AAA	GAT	ATA	CAG	AGA	CCA	GAT	6294
Leu	Gly	Glu	Asp	Leu	Thr	Leu	Asp	Leu	Lys	Asp	Ile	Gln	Arg	Pro	Asp	
			2075					2080					2085			
TCA	GAA	CAT	GGT	CTA	TCC	CCT	GAT	TCA	GAA	AAT	TTT	GAT	TGG	AAA	GCT	6342
Ser	Glu	His	Gly	Leu	Ser	Pro	Asp	Ser	Glu	Asn	Phe	Asp	Trp	Lys	Ala	
			2090				2095					2100				
ATT	CAG	GAA	GGT	GCA	AAT	TCC	ATA	GTA	AGT	AGT	TTA	CAT	CAA	GCT	GCT	6390
Ile	Gln	Glu	Gly	Ala	Asn	Ser	Ile	Val	Ser	Ser	Leu	His	Gln	Ala	Ala	
			2105			2110					2115					
GCT	GCT	GCA	TGT	TTA	TCT	AGA	CAA	GCT	TCG	TCT	GAT	TCA	GAT	TCC	ATC	6438
Ala	Ala	Ala	Cys	Leu	Ser	Arg	Gln	Ala	Ser	Ser	Asp	Ser	Asp	Ser	Ile	
			2120			2125				2130					2135	
CTT	TCC	CTG	AAA	TCA	GGA	ATC	TCT	CTG	GGA	TCA	CCA	TTT	CAT	CTT	ACA	6486
Leu	Ser	Leu	Lys	Ser	Gly	Ile	Ser	Leu	Gly	Ser	Pro	Phe	His	Leu	Thr	
				2140					2145					2150		
CCT	GAT	CAA	GAA	GAA	AAA	CCC	TTT	ACA	AGT	AAT	AAA	GGC	CCA	CGA	ATT	6534
Pro	Asp	Gln	Glu	Glu	Lys	Pro	Phe	Thr	Ser	Asn	Lys	Gly	Pro	Arg	Ile	
				2155				2160					2165			
CTA	AAA	CCA	GGG	GAG	AAA	AGT	ACA	TTG	GAA	ACT	AAA	AAG	ATA	GAA	TCT	6582
Leu	Lys	Pro	Gly	Glu	Lys	Ser	Thr	Leu	Glu	Thr	Lys	Lys	Ile	Glu	Ser	
			2170				2175						2180			
GAA	AGT	AAA	GGA	ATC	AAA	GGA	GGA	AAA	AAA	GTT	TAT	AAA	AGT	TTG	ATT	6630
Glu	Ser	Lys	Gly	Ile	Lys	Gly	Gly	Lys	Lys	Val	Tyr	Lys	Ser	Leu	Ile	
			2185			2190				2195						
ACT	GGA	AAA	GTT	CGA	TCT	AAT	TCA	GAA	ATT	TCA	GGC	CAA	ATG	AAA	CAG	6678
Thr	Gly	Lys	Val	Arg	Ser	Asn	Ser	Glu	Ile	Ser	Gly	Gln	Met	Lys	Gln	
			2200			2205				2210					2215	

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CCC	CTT	CAA	GCA	AAC	ATG	CCT	TCA	ATC	TCT	CGA	GGC	AGG	ACA	ATG	ATT	6726
Pro	Leu	Gln	Ala	Asn	Met	Pro	Ser	Ile	Ser	Arg	Gly	Arg	Thr	Met	Ile	
				2220					2225					2230		
CAT	ATT	CCA	GGA	GTT	CGA	AAT	AGC	TCC	TCA	AGT	ACA	AGT	CCT	GTT	TCT	6774
His	Ile	Pro	Gly	Val	Arg	Asn	Ser	Ser	Ser	Ser	Thr	Ser	Pro	Val	Ser	
			2235					2240					2245			
AAA	AAA	GGC	CCA	CCC	CTT	AAC	ACT	CCA	GCC	TCC	AAA	AGC	CCT	AGT	GAA	6822
Lys	Lys	Gly	Pro	Pro	Leu	Lys	Thr	Pro	Ala	Ser	Lys	Ser	Pro	Ser	Glu	
		2250					2255					2260				
GGT	CAA	ACA	GCC	ACC	ACT	TCT	CCT	AGA	GGA	GCC	AAG	CCA	TCT	GTG	AAA	6870
Gly	Gln	Thr	Ala	Thr	Thr	Ser	Pro	Arg	Gly	Ala	Lys	Pro	Ser	Val	Lys	
	2265					2270					2275					
TCA	GAA	TTA	AGC	CCT	GTT	GCC	AGG	CAG	ACA	TCC	CAA	ATA	GGT	GGG	TCA	6918
Ser	Glu	Leu	Ser	Pro	Val	Ala	Arg	Gln	Thr	Ser	Gln	Ile	Gly	Gly	Ser	
2280				2285				2290							2295	
AGT	AAA	GCA	CCT	TCT	AGA	TCA	GGA	TCT	AGA	GAT	TCG	ACC	CCT	TCA	AGA	6966
Ser	Lys	Ala	Pro	Ser	Arg	Ser	Gly	Ser	Arg	Asp	Ser	Thr	Pro	Ser	Arg	
				2300				2305					2310			
CCT	GCC	CAG	CAA	CCA	TTA	AGT	AGA	CCT	ATA	CAG	TCT	CCT	GGC	CGA	AAC	7014
Pro	Ala	Gln	Gln	Pro	Leu	Ser	Arg	Pro	Ile	Gln	Ser	Pro	Gly	Arg	Asn	
			2315					2320					2325			
TCA	ATT	TCC	CCT	GGT	AGA	AAT	GGA	ATA	AGT	CCT	CCT	AAC	AAA	TTA	TCT	7062
Ser	Ile	Ser	Pro	Gly	Arg	Asn	Gly	Ile	Ser	Pro	Pro	Asn	Lys	Leu	Ser	
	2330						2335					2340				
CAA	CTT	CCA	AGG	ACA	TCA	TCC	CCT	AGT	ACT	GCT	TCA	ACT	AAG	TCC	TCA	7110
Gln	Leu	Pro	Arg	Thr	Ser	Ser	Pro	Ser	Thr	Ala	Ser	Thr	Lys	Ser	Ser	
	2345					2350					2355					
GGT	TCT	GGA	AAA	ATG	TCA	TAT	ACA	TCT	CCA	GGT	AGA	CAG	ATG	AGC	CAA	7158
Gly	Ser	Gly	Lys	Met	Ser	Tyr	Thr	Ser	Pro	Gly	Arg	Gln	Met	Ser	Gln	
2360				2365					2370						2375	
CAG	AAC	CTT	ACC	AAA	CAA	ACA	GGT	TTA	TCC	AAG	AAT	GCC	AGT	AGT	ATT	7206
Gln	Asn	Leu	Thr	Lys	Gln	Thr	Gly	Leu	Ser	Lys	Asn	Ala	Ser	Ser	Ile	
			2380					2385					2390			
CCA	AGA	AGT	GAG	TCT	GCC	TCC	AAA	GGA	CTA	AAT	CAG	ATG	AAT	AAT	GGT	7254
Pro	Arg	Ser	Glu	Ser	Ala	Ser	Lys	Gly	Leu	Asn	Gln	Met	Asn	Asn	Gly	
			2395					2400					2405			
AAT	GGA	GCC	AAT	AAA	AAG	GTA	GAA	CTT	TCT	AGA	ATG	TCT	TCA	ACT	AAA	7302
Asn	Gly	Ala	Asn	Lys	Lys	Val	Glu	Leu	Ser	Arg	Met	Ser	Ser	Thr	Lys	
	2410					2415						2420				
TCA	AGT	GGA	AGT	GAA	TCT	GAT	AGA	TCA	GAA	AGA	CCT	GTA	TTA	GTA	CGC	7350
Ser	Ser	Gly	Ser	Glu	Ser	Asp	Arg	Ser	Gln	Arg	Pro	Val	Leu	Val	Arg	
	2425					2430					2435					
CAG	TCA	ACT	TTC	ATC	AAA	GAA	GCT	CCA	AGC	CCA	ACC	TTA	AGA	AGA	AAA	7398
Gln	Ser	Thr	Phe	Ile	Lys	Glu	Ala	Pro	Ser	Pro	Thr	Leu	Arg	Arg	Lys	
2440				2445					2450						2455	
TTG	GAG	GAA	TCT	GCT	TCA	TTT	GAA	TCT	CTT	TCT	CCA	TCA	TCT	AGA	CCA	7446
Leu	Glu	Glu	Ser	Ala	Ser	Phe	Glu	Ser	Leu	Ser	Pro	Ser	Ser	Arg	Pro	
			2460					2465					2470			
GCT	TCT	CCC	ACT	AGG	TCC	CAG	GCA	CAA	ACT	CCA	GTT	TTA	AGT	CCT	TCC	7494
Ala	Ser	Pro	Thr	Arg	Ser	Gln	Ala	Gln	Thr	Pro	Val	Leu	Ser	Pro	Ser	
			2475					2480					2485			
CTT	CCT	GAT	ATG	TCT	CTA	TCC	ACA	CAT	TCG	TCT	GTT	CAG	GCT	GGT	GGA	7542
Leu	Pro	Asp	Met	Ser	Leu	Ser	Thr	His	Ser	Ser	Val	Gln	Ala	Gly	Gly	
		2490					2495					2500				
TGG	CGA	AAA	CTC	CCA	CCT	AAT	CTC	AGT	CCC	ACT	ATA	GAG	TAT	AAT	GAT	7590
Trp	Arg	Lys	Leu	Pro	Pro	Asn	Leu	Ser	Pro	Thr	Ile	Glu	Tyr	Asn	Asp	
	2505					2510					2515					
GGA	AGA	CCA	GCA	AAG	CGC	CAT	GAT	ATT	GCA	CGG	TCT	CAT	TCT	GAA	AGT	7638
Gly	Arg	Pro	Ala	Lys	Arg	His	Asp	Ile	Ala	Arg	Ser	His	Ser	Glu	Ser	
2520					2525					2530				2535		

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CCT	TCT	AGA	CTT	CCA	ATC	AAT	AGG	TCA	GGA	ACC	TGG	AAA	CGT	GAG	CAC	7686
Pro	Ser	Arg	Leu	Pro	Ile	Asn	Arg	Ser	Gly	Thr	Trp	Lys	Arg	Glu	His	
				2540					2545					2550		
AGC	AAA	CAT	TCA	TCA	TCC	CTT	CCT	CGA	GTA	AGC	ACT	TGG	AGA	AGA	ACT	7734
Ser	Lys	His	Ser	Ser	Ser	Leu	Pro	Arg	Val	Ser	Thr	Trp	Arg	Arg	Thr	
			2555					2560					2565			
GGA	AGT	TCA	TCT	TCA	ATT	CTT	TCT	GCT	TCA	TCA	GAA	TCC	AGT	GAA	AAA	7782
Gly	Ser	Ser	Ser	Ser	Ile	Leu	Ser	Ala	Ser	Ser	Glu	Ser	Ser	Glu	Lys	
			2570				2575					2580				
GCA	AAA	AGT	GAG	GAT	GAA	AAA	CAT	GTG	AAC	TCT	ATT	TCA	GGA	ACC	AAA	7830
Ala	Lys	Ser	Glu	Asp	Glu	Lys	His	Val	Asn	Ser	Ile	Ser	Gly	Thr	Lys	
	2585					2590				2595						
CAA	AGT	AAA	GAA	AAC	CAA	GTA	TCC	GCA	AAA	GGA	ACA	TGG	AGA	AAA	ATA	7878
Gln	Ser	Lys	Glu	Asn	Gln	Val	Ser	Ala	Lys	Gly	Thr	Trp	Arg	Lys	Ile	
2600					2605					2610					2615	
AAA	GAA	AAT	GAA	TTT	TCT	CCC	ACA	AAT	AGT	ACT	TCT	CAG	ACC	GTT	TCC	7926
Lys	Glu	Asn	Glu	Phe	Ser	Pro	Thr	Asn	Ser	Thr	Ser	Gln	Thr	Val	Ser	
				2620				2625						2630		
TCA	GGT	GCT	ACA	AAT	GGT	GCT	GAA	TCA	AAG	ACT	CTA	ATT	TAT	CAA	ATG	7974
Ser	Gly	Ala	Thr	Asn	Gly	Ala	Glu	Ser	Lys	Thr	Leu	Ile	Tyr	Gln	Met	
			2635					2640					2645			
GCA	CCT	GCT	GTT	TCT	AAA	ACA	GAG	GAT	GTT	TGG	GTG	AGA	ATT	GAG	GAC	8022
Ala	Pro	Ala	Val	Ser	Lys	Thr	Glu	Asp	Val	Trp	Val	Arg	Ile	Glu	Asp	
			2650				2655					2660				
TGT	CCC	ATT	AAC	AAT	CCT	AGA	TCT	GGA	AGA	TCT	CCC	ACA	GGT	AAT	ACT	8070
Cys	Pro	Ile	Asn	Asn	Pro	Arg	Ser	Gly	Arg	Ser	Pro	Thr	Gly	Asn	Thr	
	2665				2670						2675					
CCC	CCG	GTG	ATT	GAC	AGT	GTT	TCA	GAA	AAG	GCA	AAT	CCA	AAC	ATT	AAA	8118
Pro	Pro	Val	Ile	Asp	Ser	Val	Ser	Glu	Lys	Ala	Asn	Pro	Asn	Ile	Lys	
2680					2685				2690						2695	
GAT	TCA	AAA	GAT	AAT	CAG	GCA	AAA	CAA	AAT	GTG	GGT	AAT	GGC	AGT	GTT	8166
Asp	Ser	Lys	Asp	Asn	Gln	Ala	Lys	Gln	Asn	Val	Gly	Asn	Gly	Ser	Val	
				2700				2705						2710		
CCC	ATG	CGT	ACC	GTG	GGT	TTG	GAA	AAT	CCG	CTG	ACC	TCC	TTT	ATT	CAG	8214
Pro	Met	Arg	Thr	Val	Gly	Leu	Glu	Asn	Arg	Leu	Thr	Ser	Phe	Ile	Gln	
			2715					2720					2725			
GTG	GAT	GCC	CCT	GAC	CAA	AAA	GGA	ACT	GAG	ATA	AAA	CCA	GGA	CAA	AAT	8262
Val	Asp	Ala	Pro	Asp	Gln	Lys	Gly	Thr	Gln	Ile	Lys	Pro	Gly	Gln	Asn	
			2730				2735					2740				
AAT	CCT	GTC	CCT	GTA	TCA	GAG	ACT	AAT	GAA	AGT	CCT	ATA	GTG	GAA	CGT	8310
Asn	Pro	Val	Pro	Val	Ser	Glu	Thr	Asn	Glu	Ser	Pro	Ile	Val	Glu	Arg	
	2745					2750					2755					
ACC	CCA	TTC	AGT	TCT	AGC	AGC	TCA	AGC	AAA	CAC	AGT	TCA	CCT	AGT	GGG	8358
Thr	Pro	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Lys	His	Ser	Ser	Pro	Ser	Gly	
	2760				2765					2770					2775	
ACT	GTT	GCT	GCC	AGA	GTG	ACT	CCT	TTT	AAT	TAC	AAC	CCA	AGC	CCT	AGG	8406
Thr	Val	Ala	Ala	Arg	Val	Thr	Pro	Phe	Asn	Tyr	Asn	Pro	Ser	Pro	Arg	
				2780					2785					2790		
AAA	AGC	AGC	GCA	GAT	AGC	ACT	TCA	GCT	CGG	CCA	TCT	CAG	ATC	CCA	ACT	8454
Lys	Ser	Ser	Ala	Asp	Ser	Thr	Ser	Ala	Arg	Pro	Ser	Gln	Ile	Pro	Thr	
			2795						2800				2805			
CCA	GTG	AAT	AAC	AAC	ACA	AAG	AAG	CGA	GAT	TCC	AAA	ACT	GAC	AGC	ACA	8502
Pro	Val	Asn	Asn	Asn	Thr	Lys	Lys	Arg	Asp	Ser	Lys	Thr	Asp	Ser	Thr	
			2810				2815					2820				
GAA	TCC	AGT	GGA	ACC	CAA	AGT	CCT	AAG	CGC	CAT	TCT	GGG	TCT	TAC	CTT	8550
Glu	Ser	Ser	Gly	Thr	Gln	Ser	Pro	Lys	Arg	His	Ser	Gly	Ser	Tyr	Leu	
	2825					2830					2835					
GTG	ACA	TCT	GTT	TAAAAGAGAG	GAAGAATGAA	ACTAAGAAAA	TTCTATGTTA									8602
Val	Thr	Ser	Val													
	2840															

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ATTACAAC	CTATATAG	ACATTTTG	TTTTC	AAATGAA	ACTTTAAA	AGACTG	AAAAATTTT	8662
GTAATAGG	TTGATTCT	TTAGAGGG	TTTGTCTG	AAGCCAT	ATTG	ATAGTATA		8722
CTTTGTCT	CTTACTG	TTTGGGAG	CACTCTTG	GGTTAGG	AAA	AAATAGAAA		8782
CCAAGTAT	GTGTACAG	TGTTTAC	ATGATTTA	AGTAGC	ATCCCA	TCCCAACT		8842
CTTAATT	ATTGCTTA	AATAATGA	ACACTAC	AGATG	GAATAT	GATATTG		8902
TTATCAAT	CTTCTAG	ATTAACT	GTACA	TACAGG	AAA	ATTGGT		8962
ATGCAAAAA	AAAATG	TTTTT	TGTCCT	TGTG	AGTCC	ATCTA	TAATCA	9022
GCTGTGAA	ATCAGTA	ATGGT	CCCG	ATGAACA	AGT	TTACCC	AGCC	9082
ACTGCATG	AATGAA	CTGAT	GGTTCA	ATTT	CAGAAG	TAA	TATGTG	9142
CATGATGT	GCATAG	ATACAG	TGTA	ATAATTT	ACA	CTATTT	TGTG	9202
AACAAAAAT	CTGTGA	ACTG	TAAAAC	ATTG	AATGAA	ACTA	TTTTAC	9262
ATCTGAA	AGTAGA	ATT	TTGCT	ATG	TGTAAT	TTGT	TGTAT	9322
GTGAGATG	GCCTTT	AT	TAATGA	GACA	TGAAT	TGT	CTCAAC	9382
CATTTCA	GAA	TAAAT	TATTG	CTGTAT	GTA	ACTG	TACTG	9442
GGTTTGT	TTTAC	ATTG	TAT	TAATTA	ATTG	TTTAA	ATGC	9502
AATTTTT	CT	TCAGC	TTCTA	TGCAT	TAA	GA	ATTTCC	9562
TGAAGA	AAGAC	TGTTG	CCACT	TAACC	ATTCC	ATGCG	TTGGC	9606
							ACTT	

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2843 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ala	Ala	Ser	Tyr	Asp	Gln	Leu	Leu	Lys	Gln	Val	Glu	Ala	Leu
1				5						10				15	
Lys	Met	Glu	Asn	Ser	Asn	Leu	Arg	Gln	Glu	Leu	Glu	Asp	Asn	Ser	Asn
			20					25					30		
His	Leu	Thr	Lys	Leu	Glu	Thr	Glu	Ala	Ser	Asn	Met	Lys	Glu	Val	Leu
		35					40					45			
Lys	Gln	Leu	Gln	Gly	Ser	Ile	Glu	Asp	Glu	Ala	Met	Ala	Ser	Ser	Gly
	50					55					60				
Gln	Ile	Asp	Leu	Leu	Glu	Arg	Leu	Lys	Glu	Leu	Asn	Leu	Asp	Ser	Ser
	65				70					75				80	
Asn	Phe	Pro	Gly	Val	Lys	Leu	Arg	Ser	Lys	Met	Ser	Leu	Arg	Ser	Tyr
				85					90					95	
Gly	Ser	Arg	Glu	Gly	Ser	Val	Ser	Ser	Arg	Ser	Gly	Glu	Cys	Ser	Pro
			100					105					110		
Val	Pro	Met	Gly	Ser	Phe	Pro	Arg	Gly	Phe	Val	Asn	Gly	Ser	Arg	
		115					120				125				
Glu	Ser	Thr	Gly	Tyr	Leu	Glu	Glu	Leu	Glu	Lys	Glu	Arg	Ser	Leu	Leu
		130				135					140				
Leu	Ala	Asp	Leu	Asp	Lys	Glu	Glu	Lys	Glu	Lys	Asp	Trp	Tyr	Tyr	Ala
	145				150				155						160
Gln	Leu	Gln	Asn	Leu	Thr	Lys	Arg	Ile	Asp	Ser	Leu	Pro	Leu	Thr	Glu
			165					170						175	
Asn	Phe	Ser	Leu	Gln	Thr	Asp	Leu	Thr	Arg	Arg	Gln	Leu	Glu	Tyr	Glu

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180										185										190									
Ala	Arg	Gln	Ile	Arg	Val	Ala	Met	Glu	Glu	Gln	Leu	Gly	Thr	Cys	Gln														
	195						200					205																	
Asp	Met	Glu	Lys	Arg	Ala	Gln	Arg	Arg	Ile	Ala	Arg	Ile	Gln	Gln	Ile														
	210					215					220																		
Glu	Lys	Asp	Ile	Leu	Arg	Ile	Arg	Gln	Leu	Leu	Gln	Ser	Gln	Ala	Thr														
	225				230					235					240														
Glu	Ala	Glu	Arg	Ser	Ser	Gln	Asn	Lys	His	Glu	Thr	Gly	Ser	His	Asp														
				245					250					255															
Ala	Glu	Arg	Gln	Asn	Glu	Gly	Gln	Gly	Val	Gly	Glu	Ile	Asn	Met	Ala														
			260					265					270																
Thr	Ser	Gly	Asn	Gly	Gln	Gly	Ser	Thr	Thr	Arg	Met	Asp	His	Glu	Thr														
		275					280					285																	
Ala	Ser	Val	Leu	Ser	Ser	Ser	Ser	Thr	His	Ser	Ala	Pro	Arg	Arg	Leu														
	290					295					300																		
Thr	Ser	His	Leu	Gly	Thr	Lys	Val	Glu	Met	Val	Tyr	Ser	Leu	Leu	Ser														
	305				310				315					320															
Met	Leu	Gly	Thr	His	Asp	Lys	Asp	Asp	Met	Ser	Arg	Thr	Leu	Leu	Ala														
				325			330						335																
Met	Ser	Ser	Ser	Gln	Asp	Ser	Cys	Ile	Ser	Met	Arg	Gln	Ser	Gly	Cys														
			340				345					350																	
Leu	Pro	Leu	Leu	Ile	Gln	Leu	Leu	His	Gly	Asn	Asp	Lys	Asp	Ser	Val														
	355					360						365																	
Leu	Leu	Gly	Asn	Ser	Arg	Gly	Ser	Lys	Glu	Ala	Arg	Ala	Arg	Ala	Ser														
	370					375					380																		
Ala	Ala	Leu	His	Asn	Ile	Ile	His	Ser	Gln	Pro	Asp	Asp	Lys	Arg	Gly														
	385				390				395					400															
Arg	Arg	Glu	Ile	Arg	Val	Leu	His	Leu	Leu	Glu	Gln	Ile	Arg	Ala	Tyr														
				405				410					415																
Cys	Glu	Thr	Cys	Trp	Glu	Trp	Gln	Gln	Ala	His	Glu	Pro	Gly	Met	Asp														
			420				425					430																	
Gln	Asp	Lys	Asn	Pro	Met	Pro	Ala	Pro	Val	Glu	His	Gln	Ile	Cys	Pro														
	435					440					445																		
Ala	Val	Cys	Val	Leu	Met	Lys	Leu	Ser	Phe	Asp	Glu	Glu	His	Arg	His														
	450					455				460																			
Ala	Met	Asn	Glu	Leu	Gly	Gly	Leu	Gln	Ala	Ile	Ala	Glu	Leu	Leu	Gln														
	465				470				475					480															
Val	Asp	Cys	Glu	Met	Tyr	Gly	Leu	Thr	Asn	Asp	His	Tyr	Ser	Ile	Thr														
			485				490					495																	
Leu	Arg	Arg	Tyr	Ala	Gly	Met	Ala	Leu	Thr	Asn	Leu	Thr	Phe	Gly	Asp														
			500				505					510																	
Val	Ala	Asn	Lys	Ala	Thr	Leu	Cys	Ser	Met	Lys	Gly	Cys	Met	Arg	Ala														
	515						520					525																	
Leu	Val	Ala	Gln	Leu	Lys	Ser	Glu	Ser	Glu	Asp	Leu	Gln	Gln	Val	Ile														
	530					535					540																		
Ala	Ser	Val	Leu	Arg	Asn	Leu	Ser	Trp	Arg	Ala	Asp	Val	Asn	Ser	Lys														
	545				550				555					560															
Lys	Thr	Leu	Arg	Glu	Val	Gly	Ser	Val	Lys	Ala	Leu	Met	Glu	Cys	Ala														
			565				570						575																
Leu	Glu	Val	Lys	Glu	Ser	Thr	Leu	Lys	Ser	Val	Leu	Ser	Ala	Leu															
	580					585						590																	
Trp	Asn	Leu	Ser	Ala	His	Cys	Thr	Glu	Asn	Lys	Ala	Asp	Ile	Cys	Ala														
	595					600						605																	

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Val	Asp	Gly	Ala	Leu	Ala	Phe	Leu	Val	Gly	Thr	Leu	Thr	Tyr	Arg	Ser
610						615					620				
Gln	Thr	Asn	Thr	Leu	Ala	Ile	Ile	Glu	Ser	Gly	Gly	Gly	Ile	Leu	Arg
625					630					635					640
Asn	Val	Ser	Ser	Leu	Ile	Ala	Thr	Asn	Glu	Asp	His	Arg	Gln	Ile	Leu
				645					650					655	
Arg	Glu	Asn	Asn	Cys	Leu	Gln	Thr	Leu	Leu	Gln	His	Leu	Lys	Ser	His
				660				665					670		
Ser	Leu	Thr	Ile	Val	Ser	Asn	Ala	Cys	Gly	Thr	Leu	Trp	Asn	Leu	Ser
				675			680					685			
Ala	Arg	Asn	Pro	Lys	Asp	Gln	Glu	Ala	Leu	Trp	Asp	Met	Gly	Ala	Val
						695					700				
Ser	Met	Leu	Lys	Asn	Leu	Ile	His	Ser	Lys	His	Lys	Met	Ile	Ala	Met
705					710					715					720
Gly	Ser	Ala	Ala	Ala	Leu	Arg	Asn	Leu	Met	Ala	Asn	Arg	Pro	Ala	Lys
				725					730					735	
Tyr	Lys	Asp	Ala	Asn	Ile	Met	Ser	Pro	Gly	Ser	Ser	Leu	Pro	Ser	Leu
				740				745					750		
His	Val	Arg	Lys	Gln	Lys	Ala	Leu	Glu	Ala	Glu	Leu	Asp	Ala	Gln	His
				755			760					765			
Leu	Ser	Glu	Thr	Phe	Asp	Asn	Ile	Asp	Asn	Leu	Ser	Pro	Lys	Ala	Ser
					775						780				
His	Arg	Ser	Lys	Gln	Arg	His	Lys	Gln	Ser	Leu	Tyr	Gly	Asp	Tyr	Val
785					790					795					800
Phe	Asp	Thr	Asn	Arg	His	Asp	Asp	Asn	Arg	Ser	Asp	Asn	Phe	Asn	Thr
				805					810					815	
Gly	Asn	Met	Thr	Val	Leu	Ser	Pro	Tyr	Leu	Asn	Thr	Thr	Val	Leu	Pro
				820				825					830		
Ser	Ser	Ser	Ser	Ser	Arg	Gly	Ser	Leu	Asp	Ser	Ser	Arg	Ser	Glu	Lys
				835			840					845			
Asp	Arg	Ser	Leu	Glu	Arg	Glu	Arg	Gly	Ile	Gly	Leu	Gly	Asn	Tyr	His
						855					860				
Pro	Ala	Thr	Glu	Asn	Pro	Gly	Thr	Ser	Ser	Lys	Arg	Gly	Leu	Gln	Ile
865					870					875					880
Ser	Thr	Thr	Ala	Ala	Gln	Ile	Ala	Lys	Val	Met	Glu	Glu	Val	Ser	Ala
				885					890					895	
Ile	His	Thr	Ser	Gln	Glu	Asp	Arg	Ser	Ser	Gly	Ser	Thr	Thr	Glu	Leu
			900					905					910		
His	Cys	Val	Thr	Asp	Glu	Arg	Asn	Ala	Leu	Arg	Arg	Ser	Ser	Ala	Ala
			915				920					925			
His	Thr	His	Ser	Asn	Thr	Tyr	Asn	Phe	Thr	Lys	Ser	Glu	Asn	Ser	Asn
						935					940				
Arg	Thr	Cys	Ser	Met	Pro	Tyr	Ala	Lys	Leu	Glu	Tyr	Lys	Arg	Ser	Ser
945					950					955					960
Asn	Asp	Ser	Leu	Asn	Ser	Val	Ser	Ser	Asn	Asp	Gly	Tyr	Gly	Lys	Arg
				965					970					975	
Gly	Gln	Met	Lys	Pro	Ser	Ile	Glu	Ser	Tyr	Ser	Glu	Asp	Asp	Glu	Ser
				980				985					990		
Lys	Phe	Cys	Ser	Tyr	Gly	Gln	Tyr	Pro	Ala	Asp	Leu	Ala	His	Lys	Ile
				995			1000					1005			
His	Ser	Ala	Asn	His	Met	Asp	Asp	Asn	Asp	Gly	Glu	Leu	Asp	Thr	Pro
						1015					1020				
Ile	Asn	Tyr	Ser	Leu	Lys	Tyr	Ser	Asp	Glu	Gln	Leu	Asn	Ser	Gly	Arg
1025					1030					1035					1040

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Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile  
 1045 1050 1055  
 Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser  
 1060 1065 1070  
 Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys  
 1075 1080 1085  
 Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser  
 1090 1095 1100  
 Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly  
 1105 1110 1115 1120  
 Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu  
 1125 1130 1135  
 Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln  
 1140 1145 1150  
 His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu  
 1155 1160 1165  
 Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala  
 1170 1175 1180  
 Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser  
 1185 1190 1195 1200  
 Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu  
 1205 1210 1215  
 Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His  
 1220 1225 1230  
 Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr  
 1235 1240 1245  
 Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val  
 1250 1255 1260  
 Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu  
 1265 1270 1275 1280  
 Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala  
 1285 1290 1295  
 Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Gly Lys Ile Gly  
 1300 1305 1310  
 Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln  
 1315 1320 1325  
 His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser  
 1330 1335 1340  
 Glu Ser Ala Arg His Lys Ala Val Glu Phe Pro Ser Gly Ala Lys Ser  
 1345 1350 1355 1360  
 Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr  
 1365 1370 1375  
 Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser  
 1380 1385 1390  
 Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu  
 1395 1400 1405  
 Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro  
 1410 1415 1420  
 Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro  
 1425 1430 1435 1440  
 Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys  
 1445 1450 1455  
 Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val

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1460					1465					1470					
Asn	Ala	Ala	Val	Gln	Arg	Val	Gln	Val	Leu	Pro	Asp	Ala	Asp	Thr	Leu
		1475					1480					1485			
Leu	His	Phe	Ala	Thr	Glu	Ser	Thr	Pro	Asp	Gly	Phe	Ser	Cys	Ser	Ser
	1490					1495					1500				
Ser	Leu	Ser	Ala	Leu	Ser	Leu	Asp	Glu	Pro	Phe	Ile	Gln	Lys	Asp	Val
1505					1510					1515				1520	
Glu	Leu	Arg	Ile	Met	Pro	Pro	Val	Gln	Glu	Asn	Asp	Asn	Gly	Asn	Glu
			1525						1530					1535	
Thr	Glu	Ser	Glu	Gln	Pro	Lys	Glu	Ser	Asn	Glu	Asn	Gln	Glu	Lys	Glu
	1540							1545					1550		
Ala	Glu	Lys	Thr	Ile	Asp	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Asp	Ser	Asp
	1555						1560					1565			
Asp	Asp	Asp	Ile	Glu	Ile	Leu	Glu	Glu	Cys	Ile	Ile	Ser	Ala	Met	Pro
1570						1575					1580				
Thr	Lys	Ser	Ser	Arg	Lys	Gly	Lys	Lys	Pro	Ala	Gln	Thr	Ala	Ser	Lys
1585					1590					1595					1600
Leu	Pro	Pro	Pro	Val	Ala	Arg	Lys	Pro	Ser	Gln	Leu	Pro	Val	Tyr	Lys
				1605					1610					1615	
Leu	Leu	Pro	Ser	Gln	Asn	Arg	Leu	Gln	Pro	Gln	Lys	His	Val	Ser	Phe
			1620					1625					1630		
Thr	Pro	Gly	Asp	Asp	Met	Pro	Arg	Val	Tyr	Cys	Val	Glu	Gly	Thr	Pro
	1635						1640					1645			
Ile	Asn	Phe	Ser	Thr	Ala	Thr	Ser	Leu	Ser	Asp	Leu	Thr	Ile	Glu	Ser
1650					1655						1660				
Pro	Pro	Asn	Glu	Leu	Ala	Ala	Gly	Glu	Gly	Val	Arg	Gly	Gly	Ala	Gln
1665					1670					1675				1680	
Ser	Gly	Glu	Phe	Glu	Lys	Arg	Asp	Thr	Ile	Pro	Thr	Glu	Gly	Arg	Ser
			1685					1690						1695	
Thr	Asp	Glu	Ala	Gln	Gly	Gly	Lys	Thr	Ser	Ser	Val	Thr	Ile	Pro	Glu
	1700						1705						1710		
Leu	Asp	Asp	Asn	Lys	Ala	Glu	Glu	Gly	Asp	Ile	Leu	Ala	Glu	Cys	Ile
	1715					1720						1725			
Asn	Ser	Ala	Met	Pro	Lys	Gly	Lys	Ser	His	Lys	Pro	Phe	Arg	Val	Lys
1730					1735						1740				
Lys	Ile	Met	Asp	Gln	Val	Gln	Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro
1745					1750					1755				1760	
Asn	Lys	Asn	Gln	Leu	Asp	Gly	Lys	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val
			1765				1770							1775	
Lys	Pro	Ile	Pro	Gln	Asn	Thr	Glu	Tyr	Arg	Thr	Arg	Val	Arg	Lys	Asn
	1780						1785						1790		
Ala	Asp	Ser	Lys	Asn	Asn	Leu	Asn	Ala	Glu	Arg	Val	Phe	Ser	Asp	Asn
	1795					1800						1805			
Lys	Asp	Ser	Lys	Lys	Gln	Asn	Leu	Lys	Asn	Asn	Ser	Lys	Asp	Phe	Asn
1810					1815						1820				
Asp	Lys	Leu	Pro	Asn	Asn	Glu	Asp	Arg	Val	Arg	Gly	Ser	Phe	Ala	Phe
1825					1830					1835				1840	
Asp	Ser	Pro	His	His	Tyr	Thr	Pro	Ile	Glu	Gly	Thr	Pro	Tyr	Cys	Phe
			1845						1850					1855	
Ser	Arg	Asn	Asp	Ser	Leu	Ser	Ser	Leu	Asp	Phe	Asp	Asp	Asp	Asp	Val
	1860						1865						1870		
Asp	Leu	Ser	Arg	Glu	Lys	Ala	Glu	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Lys
	1875						1880						1885		

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Glu Ser Glu Ala Lys Val Thr	Ser His Thr Glu Leu Thr Ser Asn Gln
1890	1895 1900
Gln Ser Ala Asn Lys Thr Glu	Ala Ile Ala Lys Gln Pro Ile Asn Arg
1905	1910 1915 1920
Gly Gln Pro Lys Pro Ile Leu	Gln Lys Gln Ser Thr Phe Pro Gln Ser
	1925 1930 1935
Ser Lys Asp Ile Pro Asp Arg	Gly Ala Ala Thr Asp Glu Lys Leu Gln
	1940 1945 1950
Asn Phe Ala Ile Glu Asn Thr	Pro Val Cys Phe Ser His Asn Ser Ser
1955	1960 1965
Leu Ser Ser Leu Ser Asp Ile	Asp Gln Glu Asn Asn Asn Lys Glu Asn
1970	1975 1980
Glu Pro Ile Lys Glu Thr Glu	Pro Pro Asp Ser Gln Gly Glu Pro Ser
1985	1990 1995 2000
Lys Pro Gln Ala Ser Gly Tyr Ala	Pro Lys Ser Phe His Val Glu Asp
	2005 2010 2015
Thr Pro Val Cys Phe Ser Arg	Asn Ser Ser Leu Ser Ser Leu Ser Ile
	2020 2025 2030
Asp Ser Glu Asp Asp Leu Leu	Gln Glu Cys Ile Ser Ser Ala Met Pro
2035	2040 2045
Lys Lys Lys Lys Pro Ser Arg	Leu Lys Gly Asp Asn Glu Lys His Ser
2050	2055 2060
Pro Arg Asn Met Gly Gly Ile Leu	Gly Glu Asp Leu Thr Leu Asp Leu
2065	2070 2075 2080
Lys Asp Ile Gln Arg Pro Asp	Ser Glu His Gly Leu Ser Pro Asp Ser
	2085 2090 2095
Glu Asn Phe Asp Trp Lys Ala Ile	Gln Glu Gly Ala Asn Ser Ile Val
2100	2105 2110
Ser Ser Leu His Gln Ala Ala	Ala Ala Ala Cys Leu Ser Arg Gln Ala
2115	2120 2125
Ser Ser Asp Ser Asp Ser Ile	Leu Ser Leu Lys Ser Gly Ile Ser Leu
2130	2135 2140
Gly Ser Pro Phe His Leu Thr	Pro Asp Gln Glu Lys Pro Phe Thr
2145	2150 2155 2160
Ser Asn Lys Gly Pro Arg Ile	Leu Lys Pro Gly Glu Lys Ser Thr Leu
	2165 2170 2175
Glu Thr Lys Lys Ile Glu Ser	Gln Ser Lys Gly Ile Lys Gly Gly Lys
2180	2185 2190
Lys Val Tyr Lys Ser Leu Ile	Thr Gly Lys Val Arg Ser Asn Ser Glu
2195	2200 2205
Ile Ser Gly Gln Met Lys Gln	Pro Leu Gln Ala Asn Met Pro Ser Ile
2210	2215 2220
Ser Arg Gly Arg Thr Met Ile	His Ile Pro Gly Val Arg Asn Ser Ser
2225	2230 2235 2240
Ser Ser Thr Ser Pro Val Ser	Lys Lys Gly Pro Pro Leu Lys Thr Pro
	2245 2250 2255
Ala Ser Lys Ser Pro Ser Glu	Gly Gln Thr Ala Thr Thr Ser Pro Arg
2260	2265 2270
Gly Ala Lys Pro Ser Val Lys	Ser Glu Leu Ser Pro Val Ala Arg Gln
2275	2280 2285
Thr Ser Gln Ile Gly Gly Ser	Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser
2290	2295 2300
Arg Asp Ser Thr Pro Ser Arg	Pro Ala Gln Gln Pro Leu Ser Arg Pro
2305	2310 2315 2320

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Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile  
 2325 2330 2335  
 Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser  
 2340 2345 2350  
 Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser  
 2355 2360 2365  
 Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu  
 2370 2375 2380  
 Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly  
 2385 2390 2395 2400  
 Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu  
 2405 2410 2415  
 Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser  
 2420 2425 2430  
 Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro  
 2435 2440 2445  
 Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser  
 2450 2455 2460  
 Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln  
 2465 2470 2475 2480  
 Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His  
 2485 2490 2495  
 Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser  
 2500 2505 2510  
 Pro Thr Ile Glu Tyr Asn Asn Gly Arg Pro Ala Lys Arg His Asp Ile  
 2515 2520 2525  
 Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser  
 2530 2535 2540  
 Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg  
 2545 2550 2555 2560  
 Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala  
 2565 2570 2575  
 Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val  
 2580 2585 2590  
 Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala  
 2595 2600 2605  
 Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn  
 2610 2615 2620  
 Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser  
 2625 2630 2635 2640  
 Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp  
 2645 2650 2655  
 Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly  
 2660 2665 2670  
 Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu  
 2675 2680 2685  
 Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln  
 2690 2695 2700  
 Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn  
 2705 2710 2715 2720  
 Arg Leu Thr Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr  
 2725 2730 2735  
 Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn

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2740						2745						2750					
Glu	Ser	Pro	Ile	Val	Glu	Arg	Thr	Pro	Phe	Ser	Ser	Ser	Ser	Ser	Ser		
2755						2760						2765					
Lys	His	Ser	Ser	Pro	Ser	Gly	Thr	Val	Ala	Ala	Arg	Val	Thr	Pro	Phe		
2770						2775						2780					
Asn	Tyr	Asn	Pro	Ser	Pro	Arg	Lys	Ser	Ser	Ala	Asp	Ser	Thr	Ser	Ala		
2785						2790						2795					
Arg	Pro	Ser	Gln	Ile	Pro	Thr	Pro	Val	Asn	Asn	Asn	Thr	Lys	Lys	Arg		
2805						2810						2815					
Asp	Ser	Lys	Thr	Asp	Ser	Thr	Glu	Ser	Ser	Gly	Thr	Gln	Ser	Pro	Lys		
2820						2825						2830					
Arg	His	Ser	Gly	Ser	Tyr	Leu	Val	Thr	Ser	Val							
2835						2840											

GCA Ala 1	GTC Val	GCC Ala	GCT Ala	CCA Pro 5	GTC Val	TAT Tyr	CCG Pro	GCA Ala	CTA Leu 10	GGA Gly	ACA Thr	GCC Ala	CCG Pro	GGN Gly 15	GGC Gly	48
GAG Glu	ACG Thr	GTC Val	CCC Pro 20	GCC Ala	ATG Met	TCT Ser	GCG Ala	GCC Ala	ATG Met 25	AGG Arg	GAG Glu	AGG Arg	TTC Phe 30	GAC Asp	CGG Arg	96
TTC Phe	CTG Leu	CAC His 35	GAG Glu	AAG Lys	AAC Asn	TGC Cys	ATG Met 40	ACT Thr	GAC Asp	CTT Leu	CTG Leu	GCC Ala 45	AAG Lys	CTC Leu	GAG Glu	144
GCC Ala	AAA Lys 50	ACC Thr	GGC Gly	GTG Val	AAC Asn 55	AGG Arg	AGC Ser	TTC Phe	ATC Ile	GCT Ala 60	CTT Leu 65	GGT Gly	GTC Val	ATC Ile	GGA Gly	192
CTG Leu 65	GTG Val	GCC Ala	TTG Leu	TAC Tyr 70	CTG Leu 75	GTG Val	TTC Phe	GGT Gly	TAT Tyr 80	GGA Gly 85	GCC Ala	TCT Ser	CTC Leu	CTC Leu	TGC Cys 90	240
AAC Asn	CTG Leu	ATA Ile	GGA Gly	TTT Phe 85	GGC Gly	TAC Tyr	CCA Pro	GCC Ala	TAC Tyr 90	ATC Ile	TCA Ser	ATT Ile	AAA Lys	GCT Ala 95	ATA Ile	288
GAG Glu	AGT Ser	CCC Pro	AAC Asn 100	AAA Lys	GAA Glu	GAT Asp	GAT Asp	ACC Thr 105	CAG Gln	TGG Trp	CTG Leu	ACC Thr	TAC Tyr	TGG Trp	GTA Val	336
GTG Val	TAT Tyr	GGT Gly 115	GTG Val	TTC Phe	AGC Ser	ATT Ile	GCT Ala 120	GAA Glu	TTC Phe	TTC Phe	TCT Ser	GAT Asp 125	ATC Ile	TTC Phe	CTG Leu	384
TCA Ser	TGG Trp 130	TTC Phe	CCC Pro	TTC Phe	TAC Tyr	TAC Tyr 135	ATG Met	CTG Leu	AAG Lys	TGT Cys	GGC Gly 140	TTC Phe	CTG Leu	TTG Leu	TGG Trp	432
TGC Val	ATG Tyr	GCC Ala	CCG Pro	AGC Ser	CCT Pro	TCT Ser	AAT Asn	GGG Gly	GCT Ala	GAA Gln	CTG Leu	CTC Leu	TAC Tyr	AAG Lys	CGC Arg	480

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Cys 145	Met	Ala	Pro	Ser	Pro 150	Ser	Asn	Gly	Ala	Glu 155	Leu	Leu	Tyr	Lys	Arg 160	
ATC	ATC	CGT	CCT	TTC	TTC	CTG	AAG	CAC	GAG	TCC	CAG	ATG	GAC	AGT	GTG	528
Ile	Ile	Arg	Pro	Phe	Phe	Leu	Lys	His	Glu	Ser	Gln	Met	Asp	Ser	Val	
				165					170					175		
GTC	AAG	GAC	CTT	AAA	GAC	AAG	TCC	AAA	GAG	ACT	GCA	GAT	GCC	ATC	ACT	576
Val	Lys	Asp	Leu	Lys	Asp	Lys	Ser	Lys	Glu	Thr	Ala	Asp	Ala	Ile	Thr	
			180					185					190			
AAA	GAA	GCG	AAG	AAA	GCT	ACC	GTG	AAT	TTA	CTG	GGT	GAA	GAA	AAG	AAG	624
Lys	Glu	Ala	Lys	Lys	Ala	Thr	Val	Asn	Leu	Leu	Gly	Glu	Glu	Lys	Lys	
			195				200					205				
AGC	ACC	TAA	ACC	CAG	CAC	TAA	ACC	CAG	CAC	TGG	ATG	GAAA	CTT	CCT	GCCC	680
Ser	Thr															
															210	
TTC	CTA	CTG	AG	CTT	GAT	GTT	TAT	ATT	AGG	GG	ACT	TG	GGT	TAT	AATT	740
CTT	GGA	ACA	TTTT	TG	AGAT	ATT	AAAA	AGATT	GGA	ATG	TGT	GTT	CTA	TCT	TTG	800
TTA	CTG	TCTA	TAT	ATAT	AGG	GAG	CAC	TTTA	AAC	TAA	TGC	AGT	GGG	CAGT	GTCC	860
TTG	GAAA	ATG	TAT	TTT	GCCT	CTG	GT	AGGA	AA	AGAT	GTAT	GTT	GCT	ATCC	TGC	920
ATA	AACT	TAA	AATA	AAATTA	TAT	AC	CCAC	AGG	CTG	TGTA	CTT	ACT	GGG	CTC	TCC	980
ACG	SAT	TTTC	TCT	GTA	GTTA	CAT	TAG	GRT	AAT	CTT	TATG	GTT	CTA	CTT	C	1040
CA	ATTT	TATA	TA	ATTC	NGRA	AT	GTTTT	TAA	TG	TATTT	TGTG	CAC	ATG	TACA	TAT	1100
TTA	CTG	TCTG	ACT	AC	ANCAT	GC	ATCAT	GCT	CAT	GGG	GAGG	GAG	CAG	GGGA	AGG	1160
TGT	CAT	TTAT	AACT	TCT	GTA	CAG	TA	AGACC	ACCT	GCCAAA	AGCT	GGA	GGGA	ACC	ATT	1220
TGG	TGT	GGTC	TACT	AA	ATAA	TACT	TTA	AGGA	AAT	ACGT	GAT	TAAT	ATG	CAA	GTG	1280
TG	AGAA	ATGA	AAT	CGA	ATGG	AG	ATTG	GCCT	GGT	TGTTT	TCC	GTA	G	TATAT	G	1340
ACC	AGG	ATAG	CTTT	ATA	AAAG	CAG	T	AGTTA	GTT	AGTT	ACT	CAC	TCT	AGTG	ATA	1400
AA	ATTT	TACAC	AC	AC	ACACAC	AC	AC	ACACAC	AC	AC	ACACAC	AC	AC	ACACAC	AC	1460
AGT	ACC	CTGT	AACT	CT	CAAT	TCC	CT	GAAAA	AC	AGTA	ATA	CTG	TCT	TATC	TG	1520
TTT	AC	ATATT	TG	TCT	ATTGT	CA	AGAT	GCTA	CAN	TGG	AMNC	CAT	TTCT	GGT	TTT	1580
NAG	SGG	AGAN	AC	ATG	TGAT	TT	AGT	CTTCT	TT	CC	ATCT	TCT	TTTT	TTAA	MCC	1640
GGM	NCT	TCTG	RAG	ATTG	Y C	CAC	CT	CTGAT	TAC	ATG	TATG	TTCT	Y	GTTG	TAT	1700
AAC	A	CATGC	TAAT	GRC	GAC	AC	CT	AGCTGT	RA	MG	CAATT	CTG	GGG	AGANT	GAR	1760
ATA	RAG	TMNC	CC	ATA	ATCTG	CTT	GG	CAATA	GT	TAA	GTCAA	TCT	ATC	TTCA	GTT	1820
GGC	CTTT	TAAG	GT	CAA	ACACA	AG	AGG	CTTCC	CT	AGTT	TACA	AGT	CAG	AGTC	ACT	1880
CAT	TTAA	ATG	CC	CT	CATCCG	TAT	TCT	TTTGT	GT	AG	TAAAC	TGC	ACA	KGAC	TAC	1940
GT	AC	AGANCA	GT	AA	AGTTAA	NN	CG	ATGTC	TCC	ATT	GATC	TG	CCA	ANTCG	NT	2000
CA	ATTT	TGTCT	GG	ACT	AGAAA	AT	CT	GAGTTT	TAC	ACC	CATAC	TG	TAA	AGAGT	CCT	2060
TAA	ACT	AGAC	TAAA	ACA	AGT	GT	ATA	ACTAA	ACT	A	CAAGA	TTAA	A	TATCC	AG	2120
GT	ATTT	TTTTTA	AGG	CAA	ATAA	AG	AT	GATTAG	CT	CAC	CTTG	ONT	A	CAATC	AGG	2180
AT	NACA	ATGT	CT	CAT	GATGT	NA	ANA	ATATT	AA	AG	ATATCA	ATA	CTA	AGTG	ACA	2240
NN	CTA	ATATA	AT	ATG	GATCA	GAG	CAT	TTTAT	TTT	G	GGGAGG	AAA	A	CAGTGG	TG	2300
CAT	TTT	TATTA	AACT	TAAA	AAC	TTT	G	TAGAAA	G	CAA	ACAAAA	TTG	TCT	TTGG	GAG	2360
ACT	TTT	TAGAT	TAAAA	AAAA	ATT	T	TA	AGTAWCT	AGG	AGT	ATTT	AAAT	C	TTTT	CCC	2420
AA	AGT	ACAGT	TTT	CTT	GGTG	GC	AGA	ATGAA	AAT	CAG	CAAC	NT	CTA	GCATA	TAG	2480
AAT	CAG	ATTG	AC	AG	CATATA	GA	AT	TATATTA	TC	AG	ACAAGA	TG	AGG	AGTA	CAAA	2540

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TATTGCTCAT AATGACTTAC AGGCTAAAA TAGNTNTAAA ATACTATATT AAATTCTGAA 2600  
TGCAATTTTT TTTTGTTCCT TTGAGACCAA AATTTAAGTT AACTGTTGCT GGCAGTCTAA 2660  
GTGTAAATGT TAACAGCAGG AGAAGTTAAG AATTGAGCAG TTCTGTTGCA TGATTTCCTCA 2720  
AATGAAATAC TGCCTTGGCT AGAGTTTGAA AAACATAATTG AGCCTGTGCC TGGCTAGAAA 2780  
ACAAGCGTIT ATTTGAATGT GAATAGTGTT TCAAAGGTAT GTAGTTACAG AATTCCTACC 2840  
AAACAGCTTA AATTCTTCAA QAAAGAATTG CTGCAGCAGT TATTCCTTA CCTGAAGGCT 2900  
TCAATCATTT GGATCAACAA CTGCTACTCT CGGGAAGACT CCTCTACTCA CAGCTGAAGA 2960  
AAATGAGCAC ACCCTTCACA CTGTTATCAC CTATCCTGAA GATGTGATAC ACTGAATGGA 3020  
AATAAATAGA TGTAATAAAA ATTGAGWTCT CATTAAAAA AAACCATGTG CCCAATGGGA 3080  
AAATGACCTC ATGTTGTGGT TTAACAGCA ACTGCACCCA CTAGCACAGC CCATTGAGCT 3140  
ANCCTATATA TACATCTCTG TCAGTCCCCC TC 3172

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 210 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly  
1 5 10 15  
Glu Thr Val Pro Ala Met Ser Ala Ala Met Arg Glu Arg Phe Asp Arg  
20 25 30  
Phe Leu His Glu Lys Asn Cys Met Thr Asp Leu Leu Ala Lys Leu Glu  
35 40 45  
Ala Lys Thr Gly Val Asn Arg Ser Phe Ile Ala Leu Gly Val Ile Gly  
50 55 60  
Leu Val Ala Leu Tyr Leu Val Phe Gly Tyr Gly Ala Ser Leu Leu Cys  
65 70 75 80  
Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr Ile Ser Ile Lys Ala Ile  
85 90 95  
Glu Ser Pro Asn Lys Glu Asp Asp Thr Glu Trp Leu Thr Tyr Trp Val  
100 105 110  
Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu  
115 120 125  
Ser Trp Phe Pro Phe Tyr Tyr Met Leu Lys Cys Gly Phe Leu Leu Trp  
130 135 140  
Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg  
145 150 155 160  
Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Glu Met Asp Ser Val  
165 170 175  
Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr  
180 185 190  
Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys  
195 200 205  
Ser Thr  
210

## (2) INFORMATION FOR SEQ ID NO:5:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 434 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: TB1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val	Ala	Pro	Val	Val	Gly	Ser	Gly	Arg	Ala	Pro	Arg	His	Pro	Ala	1	5	10	15	
Pro	Ala	Ala	Met	His	Pro	Arg	Arg	Pro	Asp	Gly	Phe	Asp	Gly	Leu	Gly	20	25	30	
Tyr	Arg	Gly	Gly	Ala	Arg	Asp	Glu	Gln	Gly	Phe	Gly	Gly	Ala	Phe	Pro	35	40	45	
Ala	Arg	Ser	Phe	Ser	Thr	Gly	Ser	Asp	Leu	Gly	His	Trp	Val	Thr	Thr	50	55	60	
Pro	Pro	Asp	Ile	Pro	Gly	Ser	Arg	Asn	Leu	His	Trp	Gly	Glu	Lys	Ser	65	70	75	80
Pro	Pro	Tyr	Gly	Val	Pro	Thr	Thr	Ser	Thr	Pro	Tyr	Glu	Gly	Pro	Thr	85	90	95	
Glu	Glu	Pro	Phe	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Val	Gln	Gly	Gln	Ser	100	105	110	
Ser	Glu	Gln	Leu	Asn	Arg	Phe	Ala	Gly	Phe	Gly	Ile	Gly	Leu	Ala	Ser	115	120	125	
Leu	Phe	Thr	Glu	Asn	Val	Leu	Ala	His	Pro	Cys	Ile	Val	Leu	Arg	Arg	130	135	140	
Gln	Cys	Gln	Val	Asn	Tyr	His	Ala	Gln	His	Tyr	His	Leu	Thr	Pro	Phe	145	150	155	160
Thr	Val	Ile	Asn	Ile	Met	Tyr	Ser	Phe	Asn	Lys	Thr	Gln	Gly	Pro	Arg	165	170	175	
Ala	Leu	Trp	Lys	Gly	Met	Gly	Ser	Thr	Phe	Ile	Val	Gln	Gly	Val	Thr	180	185	190	
Leu	Gly	Ala	Glu	Gly	Ile	Ile	Ser	Gln	Phe	Thr	Pro	Leu	Pro	Arg	Glu	195	200	205	
Val	Leu	His	Lys	Trp	Ser	Pro	Lys	Gln	Ile	Gly	Glu	His	Leu	Leu	Leu	210	215	220	
Lys	Ser	Leu	Thr	Tyr	Val	Val	Ala	Met	Pro	Phe	Tyr	Ser	Ala	Ser	Leu	225	230	235	240
Ile	Glu	Thr	Val	Gln	Ser	Glu	Ile	Ile	Arg	Asp	Asn	Thr	Gly	Ile	Leu	245	250	255	
Glu	Cys	Val	Lys	Glu	Gly	Ile	Gly	Arg	Val	Ile	Gly	Met	Gly	Val	Pro	260	265	270	
His	Ser	Lys	Arg	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Ile	Phe	Pro	Thr	Val	275	280	285	
Leu	His	Gly	Val	Leu	His	Tyr	Ile	Ile	Ser	Ser	Val	Ile	Gln	Lys	Phe	290	295	300	
Val	Leu	Leu	Ile	Leu	Lys	Arg	Lys	Thr	Tyr	Asn	Ser	His	Leu	Ala	Glu	305	310	315	320
Ser	Thr	Ser	Pro	Val	Gln	Ser	Met	Leu	Asp	Ala	Tyr	Phe	Pro	Glu	Leu	325	330	335	
Ile	Ala	Asn	Phe	Ala	Ala	Ser	Leu	Cys	Ser	Asp	Val	Ile	Leu	Tyr	Pro				

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340	345	350
Leu Glu Thr Val Leu His Arg Leu His Ile Gln Gly Thr Arg Thr Ile		
355	360	365
Ile Asp Asn Thr Asp Leu Gly Tyr Glu Val Leu Pro Ile Asn Thr Gln		
370	375	380
Tyr Glu Gly Met Arg Asp Cys Ile Asn Thr Ile Arg Gln Glu Glu Gly		
385	390	395
Val Phe Gly Phe Tyr Lys Gly Phe Gly Ala Val Ile Ile Gln Tyr Thr		
405	410	415
Leu His Ala Ala Val Leu Gln Ile Thr Lys Ile Ile Tyr Ser Thr Leu		
420	425	430
Leu Gln		

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: YS-39(TB2)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Leu	Arg	Arg	Phe	Asp	Arg	Phe	Leu	His	Glu	Lys	Asn	Cys	Met	Thr
1				5					10					15	
Asp	Leu	Leu	Ala	Lys	Leu	Glu	Ala	Lys	Thr	Gly	Val	Asn	Arg	Ser	Phe
			20					25					30		
Ile	Ala	Leu	Gly	Val	Ile	Gly	Leu	Val	Ala	Leu	Tyr	Leu	Val	Phe	Gly
			35				40					45			
Tyr	Gly	Ala	Ser	Leu	Leu	Cys	Asn	Leu	Ile	Gly	Phe	Gly	Tyr	Pro	Ala
			50			55					60				
Tyr	Ile	Ser	Ile	Lys	Ala	Ile	Glu	Ser	Pro	Asn	Lys	Glu	Asp	Asp	Thr
			65		70				75					80	
Gln	Trp	Leu	Thr	Tyr	Trp	Val	Val	Tyr	Gly	Val	Phe	Ser	Ile	Ala	Glu
			85					90					95		
Phe	Phe	Ser	Asp	Ile	Phe	Leu	Ser	Trp	Phe	Pro	Phe	Tyr	Tyr	Ile	Leu
			100					105					110		
Lys	Cys	Gly	Phe	Leu	Leu	Trp	Cys	Met	Ala	Pro	Ser	Pro	Ser	Asn	Gly
			115				120					125			
Ala	Glu	Leu	Leu	Tyr	Lys	Arg	Ile	Ile	Arg	Pro	Phe	Phe	Leu	Lys	His
			130			135				140					
Glu	Ser	Gln	Met	Asp	Ser	Val	Val	Lys	Asp	Leu	Lys	Asp	Lys	Ala	Lys
			145		150				155					160	
Glu	Thr	Ala	Asp	Ala	Ile	Thr	Lys	Glu	Ala	Lys	Lys	Ala	Thr	Val	Asn
				165				170						175	
Leu	Leu	Gly	Glu	Glu	Lys	Lys	Ser	Thr							
			180					185							

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2842 amino acids  
 (B) TYPE: amino acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: APC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu  
1 5 10 15  
Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn  
20 25 30  
His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu  
35 40 45  
Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly  
50 55 60  
Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser  
65 70 75 80  
Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr  
85 90 95  
Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro  
100 105 110  
Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg  
115 120 125  
Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu  
130 135 140  
Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala  
145 150 155 160  
Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Leu Thr Glu Asn  
165 170 175  
Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu Ala  
180 185 190  
Arg Gln Ile Arg Val Ala Met Glu Gln Gln Leu Gly Thr Cys Gln Asp  
195 200 205  
Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu  
210 215 220  
Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu  
225 230 235 240  
Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp Ala  
245 250 255  
Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala Thr  
260 265 270  
Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr Ala  
275 280 285  
Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu Thr  
290 295 300  
Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser Met  
305 310 315 320  
Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala Met  
325 330 335  
Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys Leu  
340 345 350  
Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val Leu

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355				360				365							
Leu	Gly	Asn	Ser	Arg	Gly	Ser	Lys	Glu	Ala	Arg	Ala	Arg	Ala	Ser	Ala
	370					375					380				
Ala	Leu	His	Asn	Ile	Ile	His	Ser	Gln	Pro	Asp	Asp	Lys	Arg	Gly	Arg
385					390					395					400
Arg	Glu	Ile	Arg	Val	Leu	His	Leu	Leu	Glu	Gln	Ile	Arg	Ala	Tyr	Cys
				405					410					415	
Glu	Thr	Cys	Trp	Glu	Trp	Gln	Glu	Ala	His	Glu	Pro	Gly	Met	Asp	Gln
			420					425					430		
Asp	Lys	Asn	Pro	Met	Pro	Ala	Pro	Val	Glu	His	Gln	Ile	Cys	Pro	Ala
		435					440					445			
Val	Cys	Val	Leu	Met	Lys	Leu	Ser	Phe	Asp	Glu	Glu	His	Arg	His	Ala
	450					455					460				
Met	Asn	Glu	Leu	Gly	Gly	Leu	Gln	Ala	Ile	Ala	Glu	Leu	Leu	Gln	Val
465					470					475					480
Asp	Cys	Glu	Met	Tyr	Gly	Leu	Thr	Asn	Asp	His	Tyr	Ser	Ile	Thr	Leu
				485					490					495	
Arg	Arg	Tyr	Ala	Gly	Met	Ala	Leu	Thr	Asn	Leu	Thr	Phe	Gly	Asp	Val
			500					505					510		
Ala	Asn	Lys	Ala	Thr	Leu	Cys	Ser	Met	Lys	Gly	Cys	Met	Arg	Ala	Leu
		515					520					525			
Val	Ala	Gln	Leu	Lys	Ser	Glu	Ser	Glu	Asp	Leu	Gln	Gln	Val	Ile	Ala
	530					535					540				
Ser	Val	Leu	Arg	Asn	Leu	Ser	Trp	Arg	Ala	Asp	Val	Asn	Ser	Lys	Lys
545					550					555					560
Thr	Leu	Arg	Glu	Val	Gly	Ser	Val	Lys	Ala	Leu	Met	Glu	Cys	Ala	Leu
				565					570					575	
Glu	Val	Lys	Lys	Glu	Ser	Thr	Leu	Lys	Ser	Val	Leu	Ser	Ala	Leu	Trp
			580					585					590		
Asn	Leu	Ser	Ala	His	Cys	Thr	Glu	Asn	Lys	Ala	Asp	Ile	Cys	Ala	Val
		595					600					605			
Asp	Gly	Ala	Leu	Ala	Phe	Leu	Val	Gly	Thr	Leu	Thr	Tyr	Arg	Ser	Gln
	610					615					620				
Thr	Asn	Thr	Leu	Ala	Ile	Ile	Glu	Ser	Gly	Gly	Gly	Ile	Leu	Arg	Asn
625					630				635						640
Val	Ser	Ser	Leu	Ile	Ala	Thr	Asn	Gly	Asp	His	Arg	Gln	Ile	Leu	Arg
				645					650					655	
Glu	Asn	Asn	Cys	Leu	Gln	Thr	Leu	Leu	Gln	His	Leu	Lys	Ser	His	Ser
			660					665					670		
Leu	Thr	Ile	Val	Ser	Asn	Ala	Cys	Gly	Thr	Leu	Trp	Asn	Leu	Ser	Ala
		675					680					685			
Arg	Asn	Pro	Lys	Asp	Gln	Glu	Ala	Leu	Trp	Asp	Met	Gly	Ala	Val	Ser
	690					695					700				
Met	Leu	Lys	Asn	Leu	Ile	His	Ser	Lys	His	Lys	Met	Ile	Ala	Met	Gly
705					710					715					720
Ser	Ala	Ala	Ala	Leu	Arg	Asn	Leu	Met	Ala	Asn	Arg	Pro	Ala	Lys	Tyr
				725					730					735	
Lys	Asp	Ala	Asn	Ile	Met	Ser	Pro	Gly	Ser	Ser	Leu	Pro	Ser	Leu	His
			740					745					750		
Val	Arg	Lys	Gln	Lys	Ala	Leu	Glu	Ala	Glu	Leu	Asp	Ala	Gln	His	Leu
		755					760					765			
Ser	Glu	Thr	Phe	Asp	Asn	Ile	Asp	Asn	Leu	Ser	Pro	Lys	Ala	Ser	His
	770					775						780			

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Arg 785	Ser	Lys	Gln	Arg 790	His	Lys	Gln	Ser	Leu	Tyr 795	Gly	Asp	Tyr	Val	Phe 800
Asp	Thr	Asn	Arg 805	Asp	Asp	Asn	Arg	Ser 810	Asp	Asn	Phe	Asn	Thr 815	Gly	
Asn	Met	Thr	Val 820	Leu	Ser	Pro	Tyr	Leu 825	Asn	Thr	Thr	Val	Leu 830	Pro	Ser
Ser	Ser	Ser 835	Ser	Arg	Gly	Ser	Leu 840	Asp	Ser	Ser	Arg	Ser 845	Glu	Lys	Asp
Arg	Ser 850	Leu	Glu	Arg	Glu	Arg 855	Gly	Ile	Gly	Leu	Gly 860	Asn	Tyr	His	Pro
Ala 865	Thr	Glu	Asn	Pro	Gly 870	Thr	Ser	Ser	Lys	Arg 875	Gly	Leu	Gln	Ile	Ser 880
Thr	Thr	Ala	Ala	Gln 885	Ile	Ala	Lys	Val	Met 890	Glu	Glu	Val	Ser	Ala 895	Ile
His	Thr	Ser	Gln 900	Glu	Asp	Arg	Ser	Ser 905	Gly	Ser	Thr	Thr	Glu 910	Leu	His
Cys	Val	Thr 915	Asp	Glu	Arg	Asn	Ala 920	Leu	Arg	Arg	Ser	Ser 925	Ala	Ala	His
Thr	His 930	Ser	Asn	Thr	Tyr	Asn 935	Phe	Thr	Lys	Ser	Glu 940	Asn	Ser	Asn	Arg
Thr 945	Cys	Ser	Met	Pro	Tyr 950	Ala	Lys	Leu	Glu	Tyr 955	Lys	Arg	Ser	Ser	Asn 960
Asp	Ser	Leu	Asn	Ser 965	Val	Ser	Ser	Ser	Asp 970	Gly	Tyr	Gly	Lys	Arg 975	Gly
Gln	Met	Lys	Pro 980	Ser	Ile	Glu	Ser	Tyr 985	Ser	Glu	Asp	Asp	Glu 990	Ser	Lys
Phe	Cys	Ser 995	Tyr	Gly	Gln	Tyr	Pro	Ala 1000	Asp	Leu	Ala	His 1005	Lys	Ile	His
Ser	Ala 1010	Asn	His	Met	Asp	Asp 1015	Asn	Asp	Gly	Glu	Leu 1020	Asp	Thr	Pro	Ile
Asn 1025	Tyr	Ser	Leu	Lys	Tyr 1030	Ser	Asp	Glu	Gln	Leu 1035	Asn	Ser	Gly	Arg	Gln 1040
Ser	Pro	Ser	Gln	Asn 1045	Glu	Arg	Trp	Ala 1050	Arg	Pro	Lys	His	Ile	Ile 1055	Glu
Asp	Glu	Ile	Lys 1060	Gln	Ser	Glu	Gln	Arg 1065	Gln	Ser	Arg	Asn	Gln 1070	Ser	Thr
Thr	Tyr 1075	Pro	Val	Tyr	Thr	Glu	Ser 1080	Thr	Asp	Asp	Lys	His 1085	Leu	Lys	Phe
Gln	Pro 1090	His	Phe	Gly	Gln	Gln 1095	Glu	Cys	Val	Ser	Pro	Tyr	Arg	Ser	Arg
Gly 1105	Ala	Asn	Gly	Ser	Glu 1110	Thr	Asn	Arg	Val	Gly 1115	Ser	Asn	His	Gly	Ile 1120
Asn	Gln	Asn	Val	Ser 1125	Gln	Ser	Leu	Cys	Gln 1130	Glu	Asp	Asp	Tyr	Glu 1135	Asp
Asp	Lys	Pro	Thr 1140	Asn	Tyr	Ser	Glu	Arg 1145	Tyr	Ser	Glu	Glu	Glu 1150	Gln	His
Glu	Glu 1155	Glu	Glu	Arg	Pro	Thr	Asn 1160	Tyr	Ser	Ile	Lys	Tyr	Asn	Glu	Glu
Lys	Arg 1170	His	Val	Asp	Gln	Pro 1175	Ile	Asp	Tyr	Ser	Leu 1180	Lys	Tyr	Ala	Thr
Asp 1185	Ile	Pro	Ser	Ser	Gln 1190	Lys	Gln	Ser	Phe	Ser 1195	Phe	Ser	Lys	Ser	Ser
Ser	Gly	Gln	Ser	Ser	Lys 1205	Thr	Glu	His	Met 1210	Ser	Ser	Ser	Ser	Glu	Asn 1215

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Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His Pro  
 1220 1225 1230  
 Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys  
 1235 1240 1245  
 Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu  
 1250 1255 1260  
 Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser  
 1265 1270 1275 1280  
 Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp  
 1285 1290 1295  
 Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly Thr  
 1300 1305 1310  
 Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln His  
 1315 1320 1325  
 Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu  
 1330 1335 1340  
 Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser Pro  
 1345 1350 1355 1360  
 Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Val  
 1365 1370 1375  
 Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser Leu  
 1380 1385 1390  
 Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu Pro  
 1395 1400 1405  
 Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp  
 1410 1415 1420  
 Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro  
 1425 1430 1435 1440  
 Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys Ala  
 1445 1450 1455  
 Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val Asn  
 1460 1465 1470  
 Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu Leu  
 1475 1480 1485  
 His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser  
 1490 1495 1500  
 Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val Glu  
 1505 1510 1515 1520  
 Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu Thr  
 1525 1530 1535  
 Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala  
 1540 1545 1550  
 Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp  
 1555 1560 1565  
 Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro Thr  
 1570 1575 1580  
 Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu  
 1585 1590 1595 1600  
 Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu  
 1605 1610 1615  
 Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe Thr  
 1620 1625 1630  
 Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro Ile

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1635	1640	1645
Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro 1650 1655 1660		
Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln Ser 1665 1670 1675 1680		
Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr 1685 1690 1695		
Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu Leu 1700 1705 1710		
Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn 1715 1720 1725		
Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys Lys 1730 1735 1740		
Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro Asn 1745 1750 1755 1760		
Lys Asn Gln Leu Asp Gly Lys Lys Lys Lys Pro Thr Ser Pro Val Lys 1765 1770 1775		
Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala 1780 1785 1790		
Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn Lys 1795 1800 1805		
Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp 1810 1815 1820		
Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe Asp 1825 1830 1835 1840		
Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser 1845 1850 1855		
Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val Asp 1860 1865 1870		
Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu 1875 1880 1885		
Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln Gln 1890 1895 1900		
Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly 1905 1910 1915 1920		
Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser 1925 1930 1935		
Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn 1940 1945 1950		
Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser Leu 1955 1960 1965		
Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu 1970 1975 1980		
Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys 1985 1990 1995 2000		
Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp Thr 2005 2010 2015		
Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp 2020 2025 2030		
Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro Lys 2035 2040 2045		
Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser Pro 2050 2055 2060		

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Arg	Asn	Met	Gly	Gly	Ile	Leu	Gly	Glu	Asp	Leu	Thr	Leu	Asp	Leu	Lys	2065	2070	2075	2080
Asp	Ile	Gln	Arg	Pro	Asp	Ser	Glu	His	Gly	Leu	Ser	Pro	Asp	Ser	Glu	2085	2090	2095	
Asn	Phe	Asp	Trp	Lys	Ala	Ile	Gln	Glu	Gly	Ala	Asn	Ser	Ile	Val	Ser	2100	2105	2110	
Ser	Leu	His	Gln	Ala	Ala	Ala	Ala	Ala	Cys	Leu	Ser	Arg	Gln	Ala	Ser	2115	2120	2125	
Ser	Asp	Ser	Asp	Ser	Ile	Leu	Ser	Leu	Lys	Ser	Gly	Ile	Ser	Leu	Gly	2130	2135	2140	
Ser	Pro	Phe	His	Leu	Thr	Pro	Asp	Gln	Glu	Lys	Pro	Phe	Thr	Ser		2145	2150	2155	2160
Asn	Lys	Gly	Pro	Arg	Ile	Leu	Lys	Pro	Gly	Glu	Lys	Ser	Thr	Leu	Glu	2165	2170	2175	
Thr	Lys	Lys	Ile	Glu	Ser	Glu	Ser	Lys	Gly	Ile	Lys	Gly	Gly	Lys	Lys	2180	2185	2190	
Val	Tyr	Lys	Ser	Leu	Ile	Thr	Gly	Lys	Val	Arg	Ser	Asn	Ser	Glu	Ile	2195	2200	2205	
Ser	Gly	Gln	Met	Lys	Gln	Pro	Leu	Gln	Ala	Asn	Met	Pro	Ser	Ile	Ser	2210	2215	2220	
Arg	Gly	Arg	Thr	Met	Ile	His	Ile	Pro	Gly	Val	Arg	Asn	Ser	Ser	Ser	2225	2230	2235	2240
Ser	Thr	Ser	Pro	Val	Ser	Lys	Lys	Gly	Pro	Pro	Leu	Lys	Thr	Pro	Ala	2245	2250	2255	
Ser	Lys	Ser	Pro	Ser	Glu	Gly	Gln	Thr	Ala	Thr	Thr	Ser	Pro	Arg	Gly	2260	2265	2270	
Ala	Lys	Pro	Ser	Val	Lys	Ser	Glu	Leu	Ser	Pro	Val	Ala	Arg	Gln	Thr	2275	2280	2285	
Ser	Gln	Ile	Gly	Gly	Ser	Ser	Lys	Ala	Pro	Ser	Arg	Ser	Gly	Ser	Arg	2290	2295	2300	
Asp	Ser	Thr	Pro	Ser	Arg	Pro	Ala	Gln	Gln	Pro	Leu	Ser	Arg	Pro	Ile	2305	2310	2315	2320
Gln	Ser	Pro	Gly	Arg	Asn	Ser	Ile	Ser	Pro	Gly	Arg	Asn	Gly	Ile	Ser	2325	2330	2335	
Pro	Pro	Asn	Lys	Leu	Ser	Gln	Leu	Pro	Arg	Thr	Ser	Ser	Pro	Ser	Thr	2340	2345	2350	
Ala	Ser	Thr	Lys	Ser	Ser	Gly	Ser	Gly	Lys	Met	Ser	Tyr	Thr	Ser	Pro	2355	2360	2365	
Gly	Arg	Gln	Met	Ser	Gln	Gln	Asn	Leu	Thr	Lys	Gln	Thr	Gly	Leu	Ser	2370	2375	2380	
Lys	Asn	Ala	Ser	Ser	Ile	Pro	Arg	Ser	Glu	Ser	Ala	Ser	Lys	Gly	Leu	2385	2390	2395	2400
Asn	Gln	Met	Asn	Asn	Gly	Asn	Gly	Ala	Asn	Lys	Lys	Val	Glu	Leu	Ser	2405	2410	2415	
Arg	Met	Ser	Ser	Thr	Lys	Ser	Ser	Gly	Ser	Glu	Ser	Asp	Arg	Ser	Glu	2420	2425	2430	
Arg	Pro	Val	Leu	Val	Arg	Gln	Ser	Thr	Phe	Ile	Lys	Glu	Ala	Pro	Ser	2435	2440	2445	
Pro	Thr	Leu	Arg	Arg	Lys	Leu	Glu	Glu	Ser	Ala	Ser	Phe	Glu	Ser	Leu	2450	2455	2460	
Ser	Pro	Ser	Ser	Arg	Pro	Ala	Ser	Pro	Thr	Arg	Ser	Gln	Ala	Gln	Thr	2465	2470	2475	2480
Pro	Val	Leu	Ser	Pro	Ser	Leu	Pro	Asp	Met	Ser	Leu	Ser	Thr	His	Ser	2485	2490	2495	

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Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro  
 2500 2505 2510  
 Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile Ala  
 2515 2520 2525  
 Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly  
 2530 2535 2540  
 Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg Val  
 2545 2550 2555 2560  
 Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser  
 2565 2570 2575  
 Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val Asn  
 2580 2585 2590  
 Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala Lys  
 2595 2600 2605  
 Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser  
 2610 2615 2620  
 Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys  
 2625 2630 2635 2640  
 Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp Val  
 2645 2650 2655  
 Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg  
 2660 2665 2670  
 Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu Lys  
 2675 2680 2685  
 Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn  
 2690 2695 2700  
 Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn Arg  
 2705 2710 2715 2720  
 Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr Glu  
 2725 2730 2735  
 Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn Glu  
 2740 2745 2750  
 Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Lys  
 2755 2760 2765  
 His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe Asn  
 2770 2775 2780  
 Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg  
 2785 2790 2795 2800  
 Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg Asp  
 2805 2810 2815  
 Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg  
 2820 2825 2830  
 His Ser Gly Ser Tyr Leu Val Thr Ser Val  
 2835 2840

## ( 2 ) INFORMATION FOR SEQ ID NO:8:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 31 amino acids
- ( B ) TYPE: amino acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( ii ) MOLECULE TYPE: peptide

## ( vii ) IMMEDIATE SOURCE:

- ( B ) CLONE: ral2(yeast)

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Thr Gly Ala Lys Gly Leu Gln Leu Arg Ala Leu Arg Arg Ile Ala  
 1 5 10 15  
 Arg Ile Glu Gln Gly Gly Thr Ala Ile Ser Pro Thr Ser Pro Leu  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: m3(mACHR)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Tyr Trp Arg Ile Tyr Lys Glu Thr Glu Lys Arg Thr Lys Glu Leu  
 1 5 10 15  
 Ala Gly Leu Gln Ala Ser Gly Thr Glu Ala Glu Thr Glu  
 20 25

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: MCC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Tyr Pro Asn Leu Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu  
 1 5 10 15  
 Ala Gly Leu Arg Glu Glu Asn Glu Ser Leu Thr Ala Met  
 20 25

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATCAAGAC TGTGACTTTT AATTGTAGTT TATCCATTTT

40

## (2) INFORMATION FOR SEQ ID NO:12:

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- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 40 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
    ( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTAGAATTT CATGTTAATA TATTGTGTTT TTTTAAACAG

40

( 2 ) INFORMATION FOR SEQ ID NO:13:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 40 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
    ( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:13:

G TAGATTTTA AAAAGGTGTT TAAAAATAAT TTTTAAAGCT

40

( 2 ) INFORMATION FOR SEQ ID NO:14:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 40 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
    ( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCAATTGT TGTATAAAAA CTGTTTCTA TTTATTTAG

40

( 2 ) INFORMATION FOR SEQ ID NO:15:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 40 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
    ( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTAAC TTTTC TTCATATAGT AAACATTGCC TTGTGTACTC

40

( 2 ) INFORMATION FOR SEQ ID NO:16:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 40 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

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## ( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:16:

NNNNNNNNNN NNGTCCCTT TTTTAAAAA AAAAAATAG

40

## ( 2 ) INFORMATION FOR SEQ ID NO:17:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 40 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAAGTAACT TGGCAGTACA ACTTATTTGA AACITTAATA

40

## ( 2 ) INFORMATION FOR SEQ ID NO:18:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 40 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATACAAGATA TTGATACTTT TTTATTATTT GTGGTTTATG

40

## ( 2 ) INFORMATION FOR SEQ ID NO:19:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 40 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAAGTTACT TGTITCTAAG TGATAAAACA GYGAAGAGCT

40

## ( 2 ) INFORMATION FOR SEQ ID NO:20:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 40 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATAAAAACA TAACTAATTA GGTTTCTTGT TTTATTTTATG

40

56377" 58424460



-continued

## ( 2 ) INFORMATION FOR SEQ ID NO:21:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 40 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTTAGTAAAT TSCCTTTTTT GTTTGTGGGT ATAAAAATAG

40

## ( 2 ) INFORMATION FOR SEQ ID NO:22:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 40 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACCATTTTTG CATGTACTGA TGTTAACTCC ATCTTAACAG

40

## ( 2 ) INFORMATION FOR SEQ ID NO:23:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 40 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTAAATAAAT TATTTTATCA TATTTTTTAA AATTATTTAA

40

## ( 2 ) INFORMATION FOR SEQ ID NO:24:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 64 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CATGATGTTA TCTGTATTTA CCTATAGTCT AAATTATACC ATCTATAATG TGCTTAATTT  
TTAG

60

64

## ( 2 ) INFORMATION FOR SEQ ID NO:25:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 52 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single

52

46

40

56

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:29:

-continued

GTAAGACAAA AATGTTTTTT AATGACATAG ACAATTACTG GTG

4 3

## ( 2 ) INFORMATION FOR SEQ ID NO:30:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 40 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTAGATGATT GTCITTTTCC TCTTGCCCTT TTAAATTAG

4 0

## ( 2 ) INFORMATION FOR SEQ ID NO:31:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 44 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATGTTTT ATAACATGTA TTCTTAAGA TAGCTCAGGT ATGA

4 4

## ( 2 ) INFORMATION FOR SEQ ID NO:32:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 54 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTTGGCTTC AAGTTGNCTT TTAAATGATC CTCIATTCIG TATTTAATTT ACAAG

5 4

## ( 2 ) INFORMATION FOR SEQ ID NO:33:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 65 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTACTATTTA GAATTTACCC TGTITTTCTT TTTTCTCTTT TTCTTTGAGG CAGGGTCTCA

6 0

CTCTG

6 5

## ( 2 ) INFORMATION FOR SEQ ID NO:34:

66877" 6342460

**-continued**

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 52 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: *Homo sapiens*

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAACTAGTA TGATTTTATG TATAAATTAA TCTAAAATTG ATTAATTTCC AG

52

( 2 ) INFORMATION FOR SEQ ID NO:35:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 42 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTACCTTTGA AAACATTTAG TACTATAATA TGAATTTTCAT GT

42

( 2 ) INFORMATION FOR SEQ ID NO:36:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 40 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: *Homo sapiens*

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCAAGTCNAA TTAGATGACC CATATTCAGA AACTTACTAG

40

( 2 ) INFORMATION FOR SEQ ID NO:37:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 54 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATATAG AGTTTTATAT TACTTTTAAA GTACAGAATT CATACTCTCA AAAA

54

( 2 ) INFORMATION FOR SEQ ID NO:38:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 41 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

22  
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 1

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( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATTGTGACCT TAATTTTGTG ATCTCTTGAT TTTTATTTC A G

4 1

( 2 ) INFORMATION FOR SEQ ID NO:39:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 18 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCCCCGCGCTG CCGCTCTC

1 8

( 2 ) INFORMATION FOR SEQ ID NO:40:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 18 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCAGCGGCGG CTCCCGTG

1 8

( 2 ) INFORMATION FOR SEQ ID NO:41:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 20 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGAACGGCT CTCATGCTGC

2 0

( 2 ) INFORMATION FOR SEQ ID NO:42:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 19 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGTGCGGGG AGGAATGGA

1 9

GCGCTT "GCGCTT" (50

-continued

## ( 2 ) INFORMATION FOR SEQ ID NO:43:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 24 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGATATCTT ACCAAATGAT ATAC

2 4

## ( 2 ) INFORMATION FOR SEQ ID NO:44:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 23 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTATTCTAC TTCTTCTATA CAG

2 3

## ( 2 ) INFORMATION FOR SEQ ID NO:45:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 21 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TACCCATGCT GGCTCTTTT C

2 1

## ( 2 ) INFORMATION FOR SEQ ID NO:46:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 20 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGGGCCATC TTGTTCTGA

2 0

## ( 2 ) INFORMATION FOR SEQ ID NO:47:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 22 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

-continued

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACATTAGGCA CAAAGCTTGC AA

22

( 2 ) INFORMATION FOR SEQ ID NO:48:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 22 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCAAGCTCC AGTAAGAAGG TA

22

( 2 ) INFORMATION FOR SEQ ID NO:49:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 19 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGCGGCTCCT GGGTTGTTG

19

( 2 ) INFORMATION FOR SEQ ID NO:50:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 20 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCCCCCTTCCT TTCTGAGGAC

20

( 2 ) INFORMATION FOR SEQ ID NO:51:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 21 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTTCTCCTG CCTCTTACTG C

21

66877" 6342460

-continued

## ( 2 ) INFORMATION FOR SEQ ID NO:52:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 20 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGACACCCC CCATTCCCTC

2 0

## ( 2 ) INFORMATION FOR SEQ ID NO:53:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 24 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCACTTAAAG CACATATATT TAGT

2 4

## ( 2 ) INFORMATION FOR SEQ ID NO:54:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 22 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTATGGAAAA TAGTGAAGAA CC

2 2

## ( 2 ) INFORMATION FOR SEQ ID NO:55:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 24 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCTTAAGTC CTGTTTTTCT TTTG

2 4

## ( 2 ) INFORMATION FOR SEQ ID NO:56:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 23 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single

65877 " 6844460



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( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTTAGAACCT TTTTGTGTT GIG 23

( 2 ) INFORMATION FOR SEQ ID NO:57:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 24 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTCAGATTAT AACTAAGCC TAAC 24

( 2 ) INFORMATION FOR SEQ ID NO:58:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 22 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CATGCTCTTT ACAGTAGTAC CA 22

( 2 ) INFORMATION FOR SEQ ID NO:59:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 20 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGGTCCAAGG GTAGCCAAGG 20

( 2 ) INFORMATION FOR SEQ ID NO:60:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 27 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:60:

5691454-111-112

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TAAAAATGGA TAAACTACAA TTAAAAAG

27

## ( 2 ) INFORMATION FOR SEQ ID NO:61:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 24 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAATACAGAA TCATGCTTG AAGT

24

## ( 2 ) INFORMATION FOR SEQ ID NO:62:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 23 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ACACCTAAAG ATGACAATT GAG

23

## ( 2 ) INFORMATION FOR SEQ ID NO:63:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 24 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAACTTAGAT AGCAGTAATT TCCC

24

## ( 2 ) INFORMATION FOR SEQ ID NO:64:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 23 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Homo sapiens

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACAATAAACT GGAGTACACA AGG

23

## ( 2 ) INFORMATION FOR SEQ ID NO:65:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 23 base pairs

66977 " 11399

( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( A ) ORGANISM: *Homo sapiens*

( x i ) SEQUENCE DESCRIPTION, SEQ ID NO:65:

ATAGGTCATT GCTTCTTGCT\GAT

23

( 2 ) INFORMATION FOR SEQ ID NO:66:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 24 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TGAATTTTAA TGGATTACCT AGGT

24

( 2 ) INFORMATION FOR SEQ ID NO:67:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 25 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: *Homo sapiens*

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTTTTTTTTGC TTTTACTGAT TAACG

25

( 2 ) INFORMATION FOR SEQ ID NO:68:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 27 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: *Homo sapiens*

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TGTAATT CAT TTTATT CCTA ATAGCTC

27

( 2 ) INFORMATION FOR SEQ ID NO:69:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 24 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: *Homo sapiens*

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

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( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTAGCCATA GTATGATTAT TTCT

24

( 2 ) INFORMATION FOR SEQ ID NO:70:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 24 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTACCTATTT TTATACCCAC AAAC

24

( 2 ) INFORMATION FOR SEQ ID NO:71:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 23 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGAAAGCCT ACACCATTTT TGC

23

( 2 ) INFORMATION FOR SEQ ID NO:72:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 23 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATCATTCTT AGAACCATCT TGC

23

( 2 ) INFORMATION FOR SEQ ID NO:73:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 24 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ACCTATAGTC TAAATTATAC CATC

24

( 2 ) INFORMATION FOR SEQ ID NO:74:

668777" 66424460

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- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 20 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
    ( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTCATGGCAT TAGTGACCAG

20

( 2 ) INFORMATION FOR SEQ ID NO:75:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 24 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
    ( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:75:

AGTCGTAATT TTGTTTCTAA ACTC

24

( 2 ) INFORMATION FOR SEQ ID NO:76:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 21 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
    ( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGAAGGACTC GGATTTCACG C

21

( 2 ) INFORMATION FOR SEQ ID NO:77:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 23 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
    ( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TCATTCACTC ACAGCCTGAT GAC

23

( 2 ) INFORMATION FOR SEQ ID NO:78:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 22 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

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( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:78:  
GCTTTGAAAC ATGCACTACG AT 2 2

( 2 ) INFORMATION FOR SEQ ID NO:79:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 24 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:79:  
AAACATCATT GCTCTTCAAA TAAC 2 4

( 2 ) INFORMATION FOR SEQ ID NO:80:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 24 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:80:  
TACCATGATT TAAAAATCCA CCAG 2 4

( 2 ) INFORMATION FOR SEQ ID NO:81:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 23 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:81:  
GATGATTGTC TTTTTCCTCT TGC 2 3

( 2 ) INFORMATION FOR SEQ ID NO:82:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 24 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:82:  
CTGAGCTATC TTAAGAAATA CATG 2 4

66377 6342460

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## ( 2 ) INFORMATION FOR SEQ ID NO:83:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 25 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTTTAAATGA TCCTCTATTTC TGTAT

2 5

## ( 2 ) INFORMATION FOR SEQ ID NO:84:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 24 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACAGAGTCAG ACCCTGCCTC AAAAG

2 4

## ( 2 ) INFORMATION FOR SEQ ID NO:85:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 23 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTCTATTCT TACTGCTAGC ATT

2 3

## ( 2 ) INFORMATION FOR SEQ ID NO:86:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 22 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:  
( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATACACAGGT AAGAAATTAG GA

2 2

## ( 2 ) INFORMATION FOR SEQ ID NO:87:

- ( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 22 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

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( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TAGATGACCC ATATTCTGTT TC

2 2

( 2 ) INFORMATION FOR SEQ ID NO:88:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 22 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAATTAGGTC TTTTGTGAGAG TA

2 2

( 2 ) INFORMATION FOR SEQ ID NO:89:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 22 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTTACTGCAT ACACATTGTG AC

2 2

( 2 ) INFORMATION FOR SEQ ID NO:90:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 23 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTTTTGTGTT TCCTAACATG AAG

2 3

( 2 ) INFORMATION FOR SEQ ID NO:91:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 21 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCTCCACAG GTAATACTCC C

2 1

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## ( 2 ) INFORMATION FOR SEQ ID NO:92:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 21 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCTAGAACTG AATGGGGTAC G

2 1

## ( 2 ) INFORMATION FOR SEQ ID NO:93:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 22 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAGGACAAAA TAATCCTGTC CC

2 2

## ( 2 ) INFORMATION FOR SEQ ID NO:94:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 24 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTTTCTTAG TTTCATTCTT CCTC

2 4

## ( 2 ) INFORMATION FOR SEQ ID NO: 95:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 25 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGAAGGATCC CTTGTGCAGT GTGGA

2 5

## ( 2 ) INFORMATION FOR SEQ ID NO: 96:

- ( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 24 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single

GCTAGAACTG AATGGGGTAC G

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( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GACAGGATCC TGAAGCTGAG TTTG

24

( 2 ) INFORMATION FOR SEQ ID NO: 97:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 18 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCAGAAAAGTG CTGAAGAG

18

( 2 ) INFORMATION FOR SEQ ID NO: 98:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 19 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGAATAATTA GGCTCTCCAA

19

( 2 ) INFORMATION FOR SEQ ID NO: 99:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 21 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCAAATCCTA AGAGAGAACA A

21

( 2 ) INFORMATION FOR SEQ ID NO: 100:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 19 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:100:

**-continued**

19

( 2 ) INFORMATION FOR SEQ ID NO: 101:

( i ) SEQUENCE CHARACTERISTICS

- ( A ) LENGTH: 18 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: Homo sapiens

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:101:

18

( 2 ) INFORMATION FOR SEQ ID NO: 102:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 18 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: *Homo sapiens*

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:102:

18

[illegible]